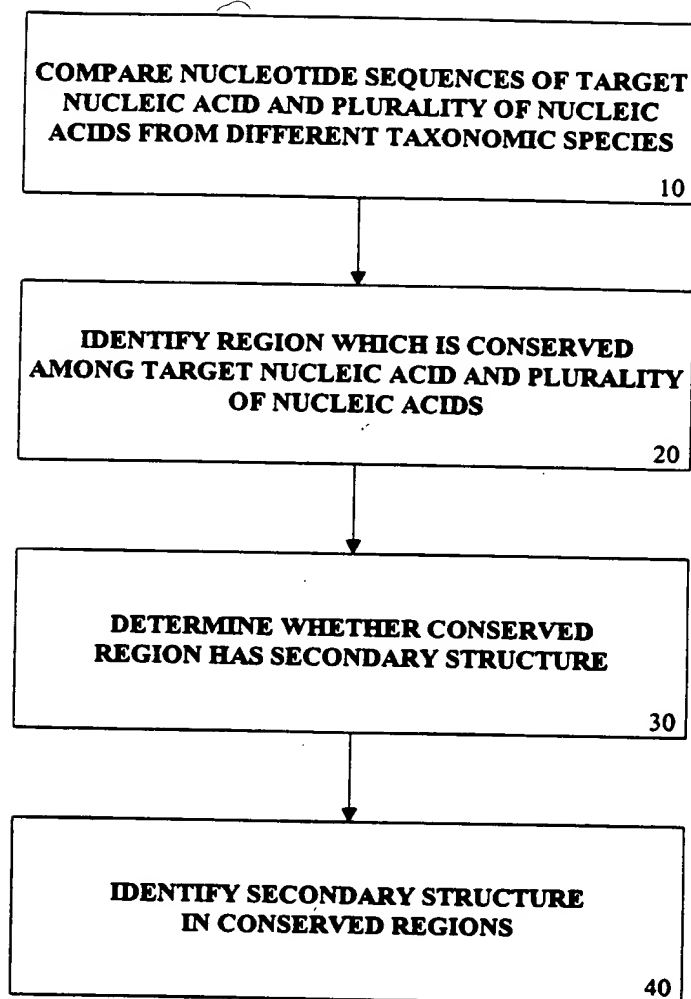


09310667.051299



**FIGURE 1**

09310567.051299  
662T50/990TE60

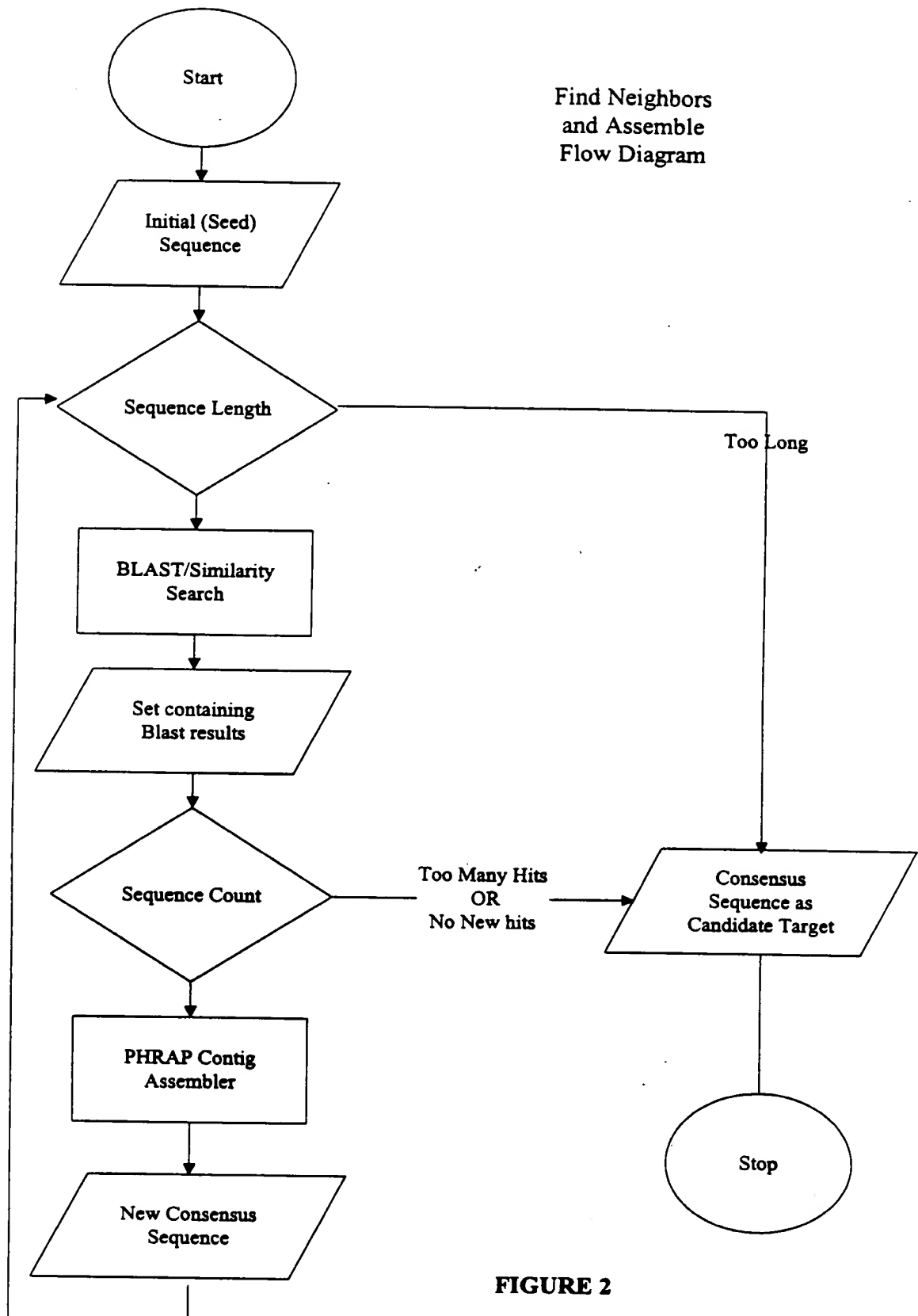


FIGURE 2

# BlastParse

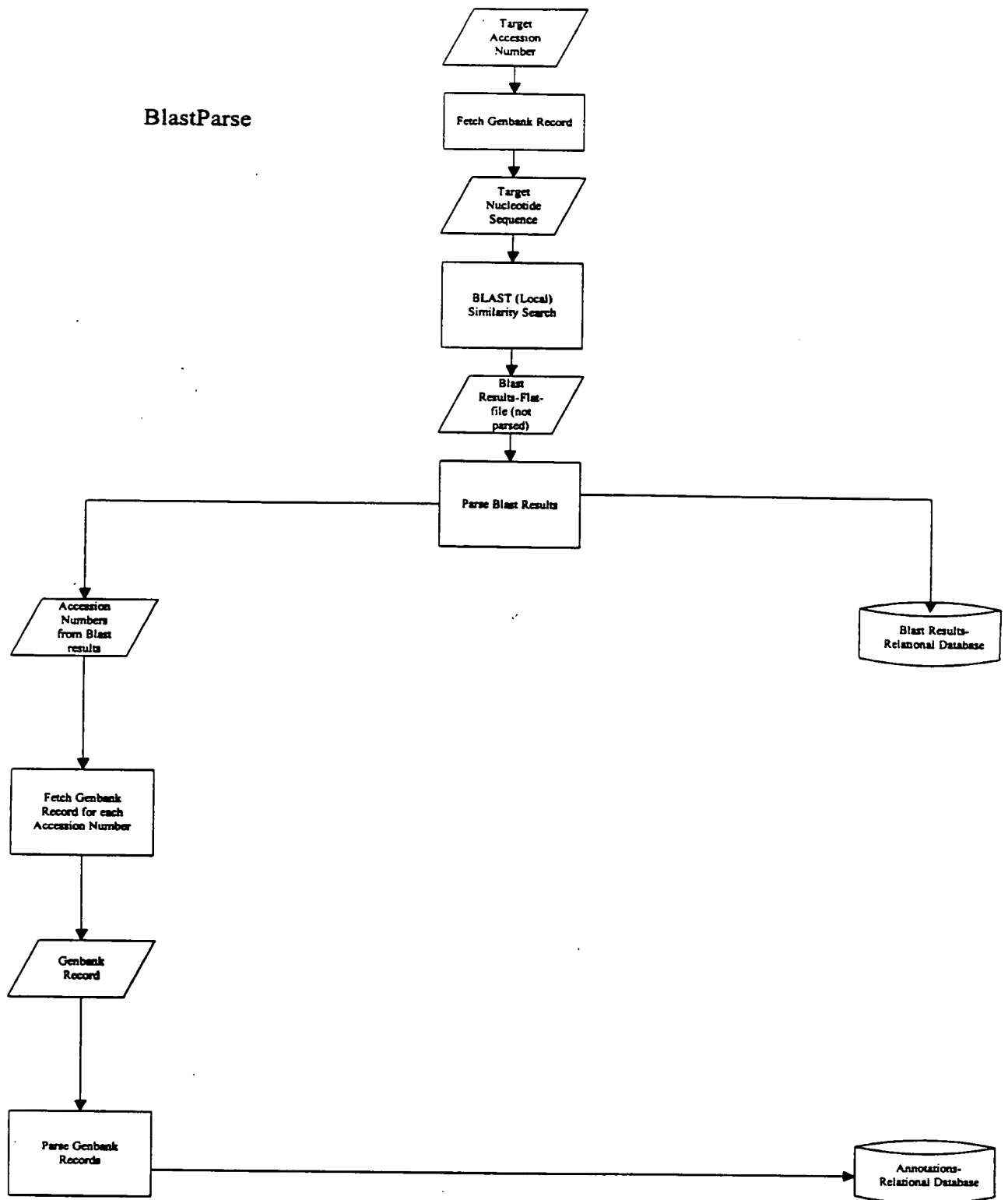


FIGURE 3

0931067.051299

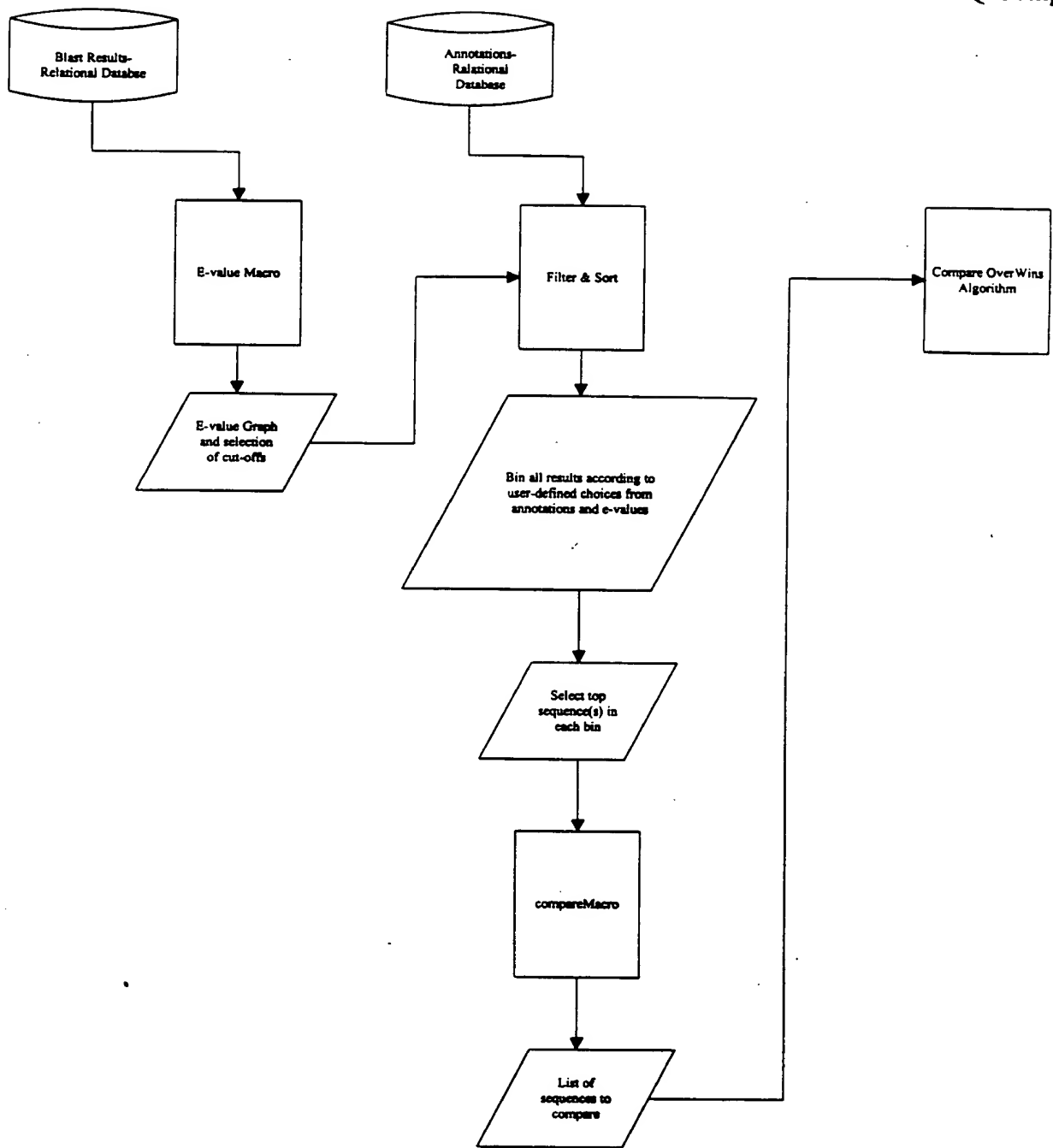


FIGURE 4

662750-2990E60

# CompareOverWins Algorithm Flow Chart

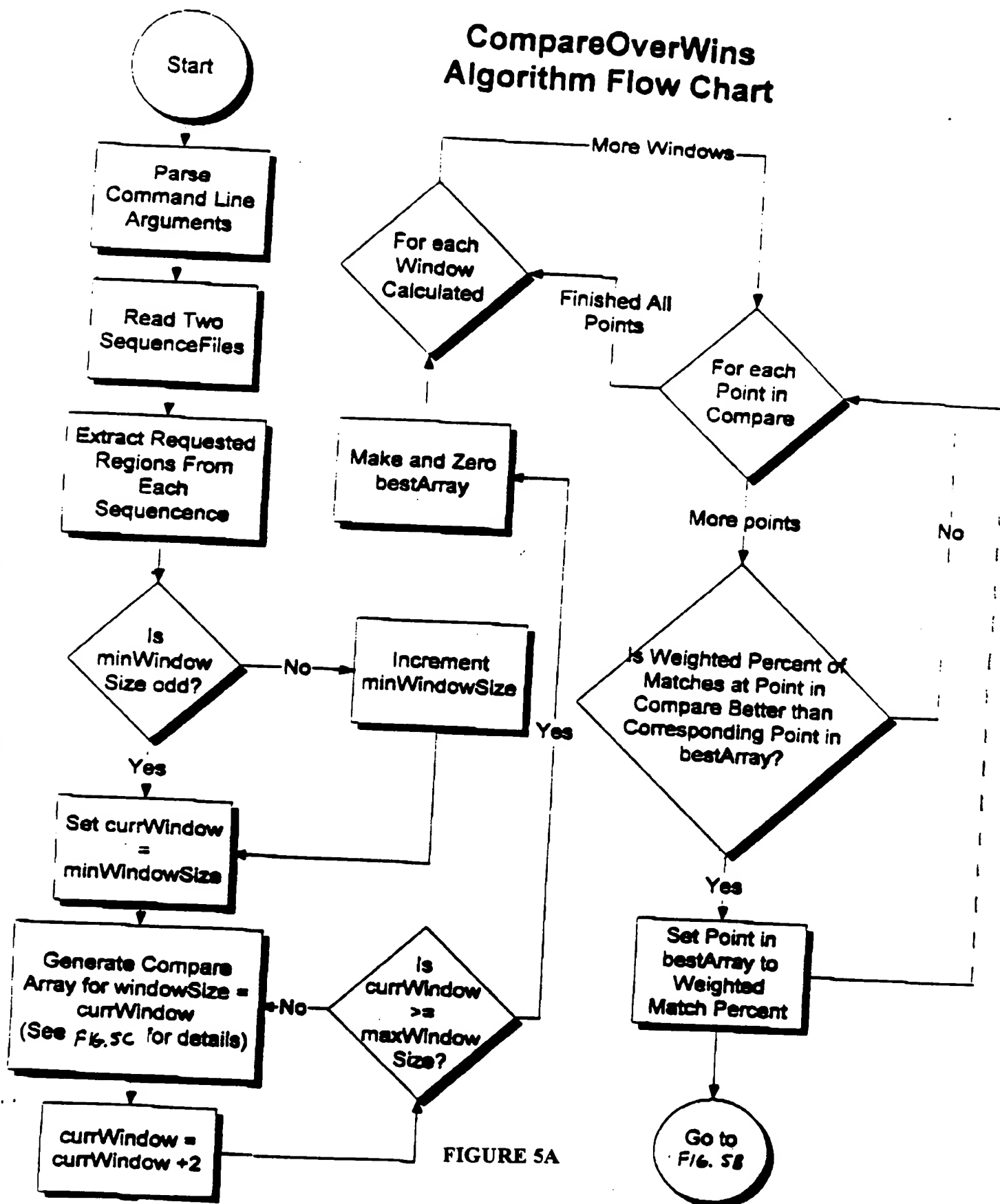
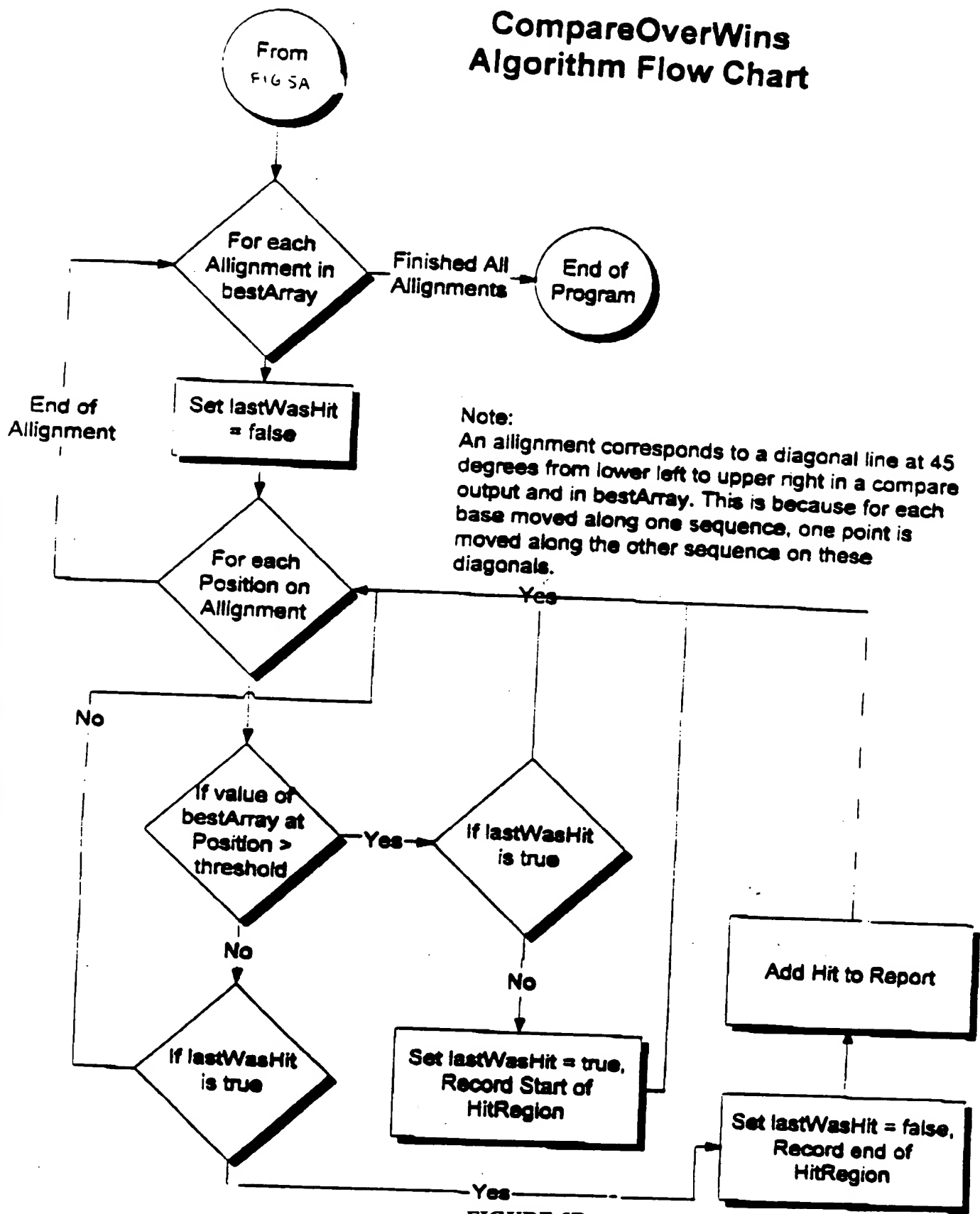


FIGURE 5A

00310667-051299

# CompareOverWins Algorithm Flow Chart



00310567 051299

# CompareOverWins Algorithm Flow Chart Basic Compare

Input:  
Sequence A length a  
Sequence B length b  
Window Size

Output:  
Array of size a by b of unsigned chars (0-255)  
Each point represents the number of matches in the  
window at that alignment and position

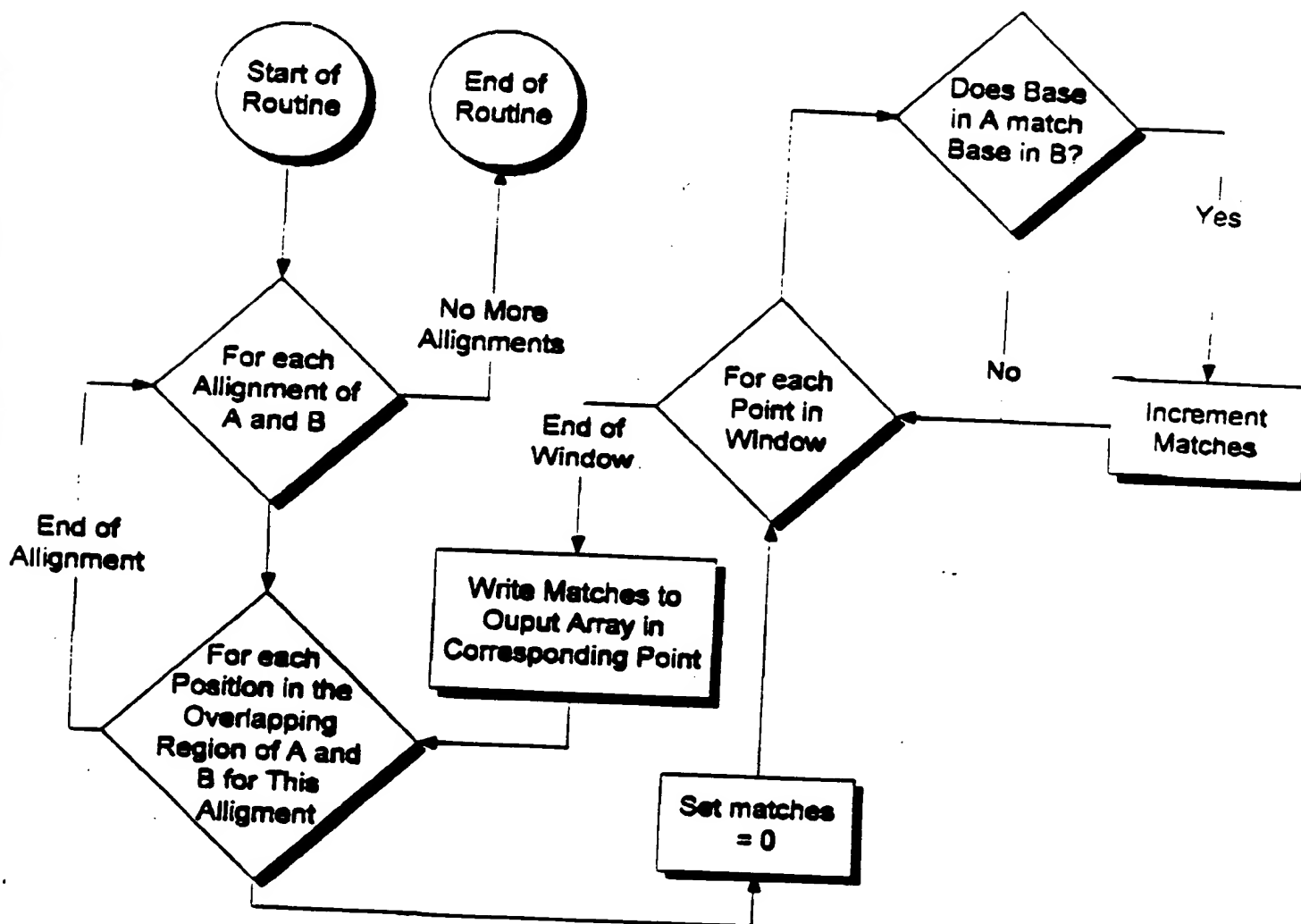
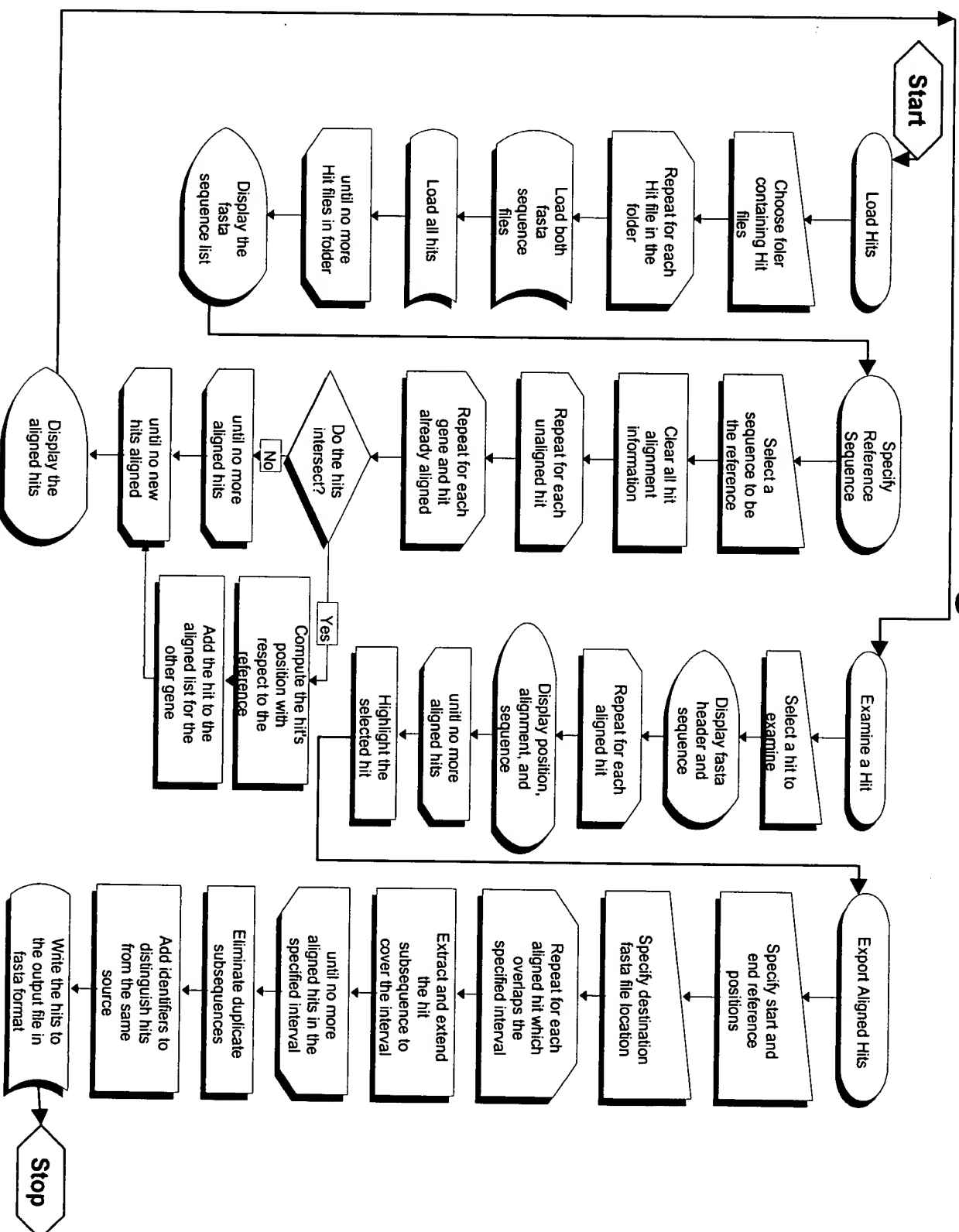


FIGURE 5C

09310667-051299

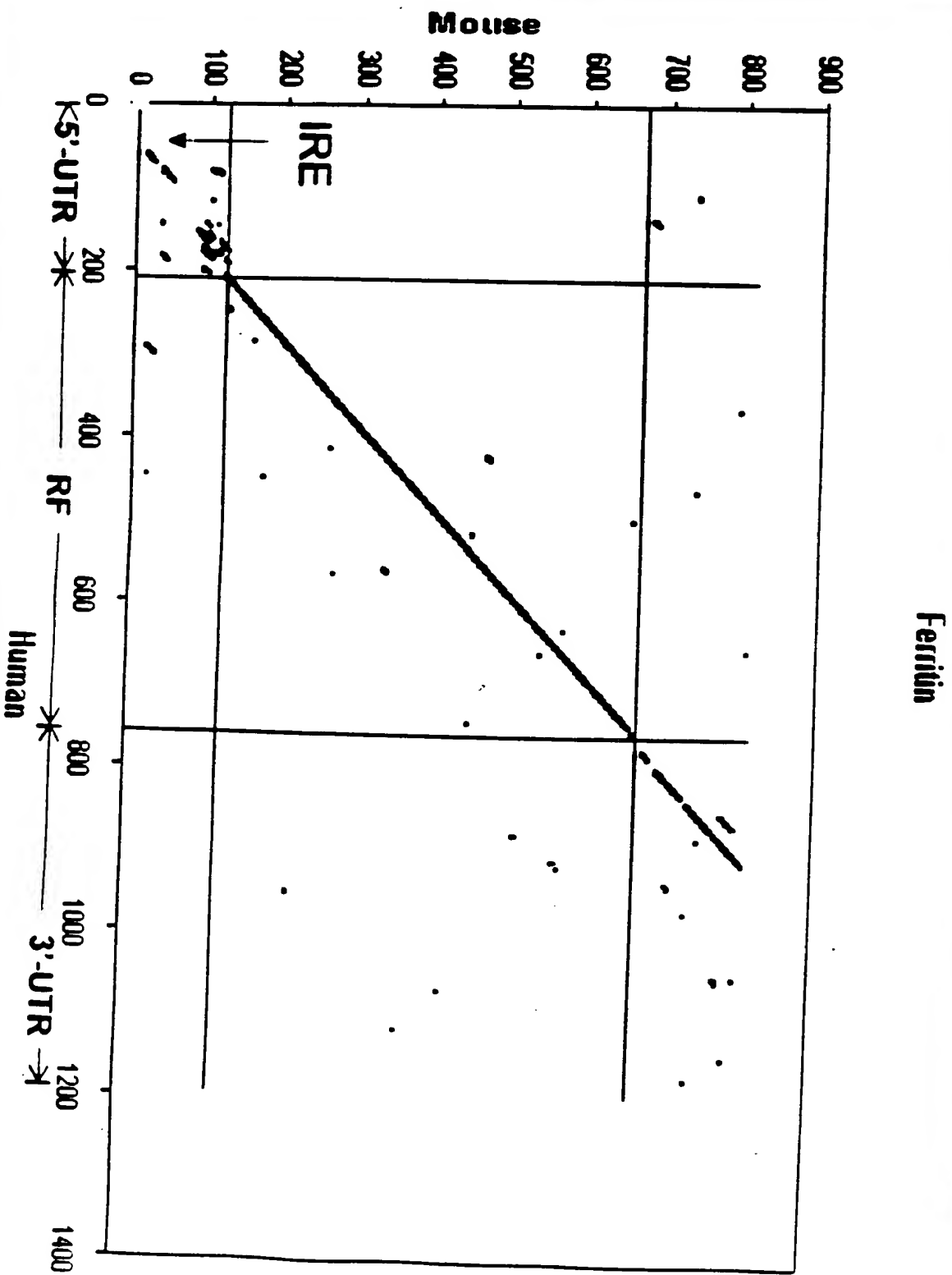
Fig. 5D



09310667.051299



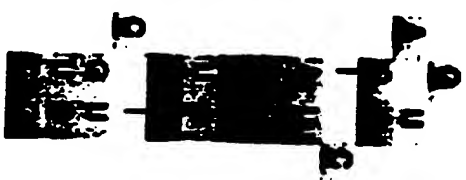
FIGURE 6



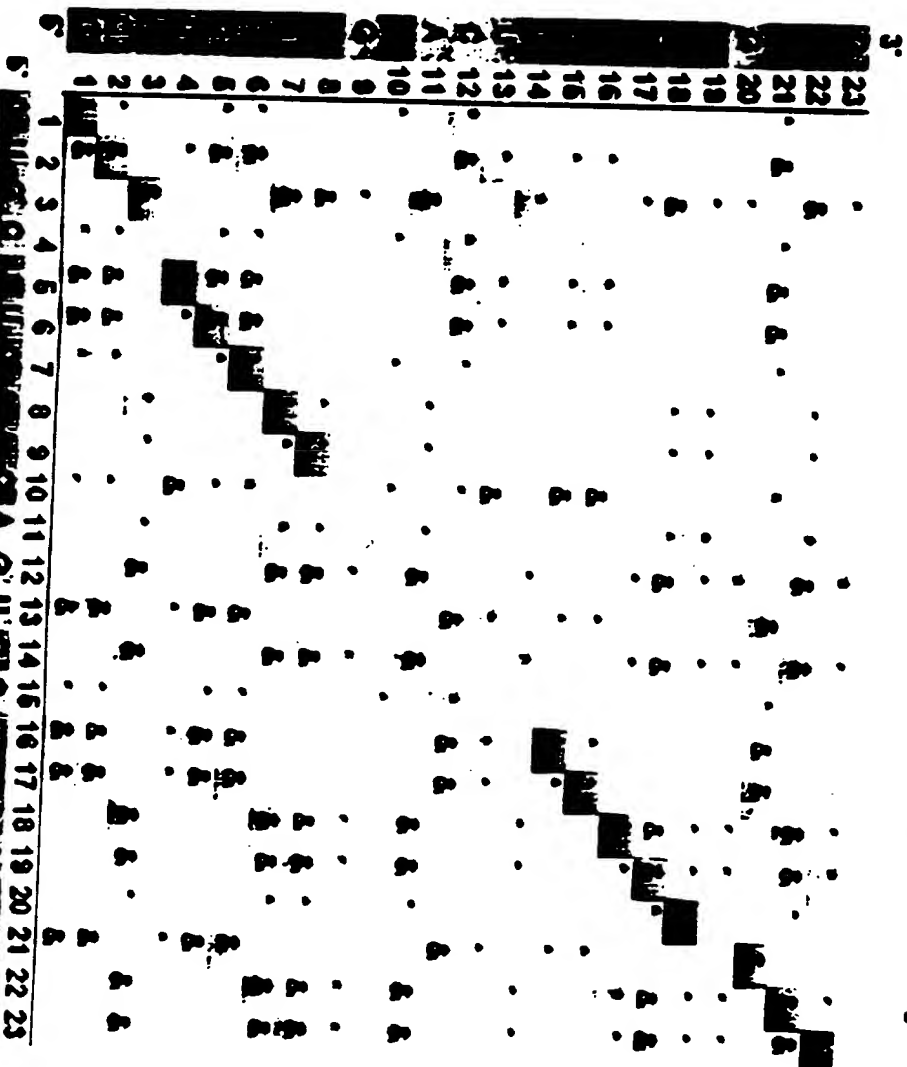
09310557 .051299

# Self Complementation Analysis - Single Sequence

FIGURE 7



X Y  
C C  
G G  
A A  
U U  
C C



1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23  
5' C U G C U U G A C A G U G C U U G A U U G C 3'  
23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

# Self Complementarity Comparisons 13 ortholog overlay

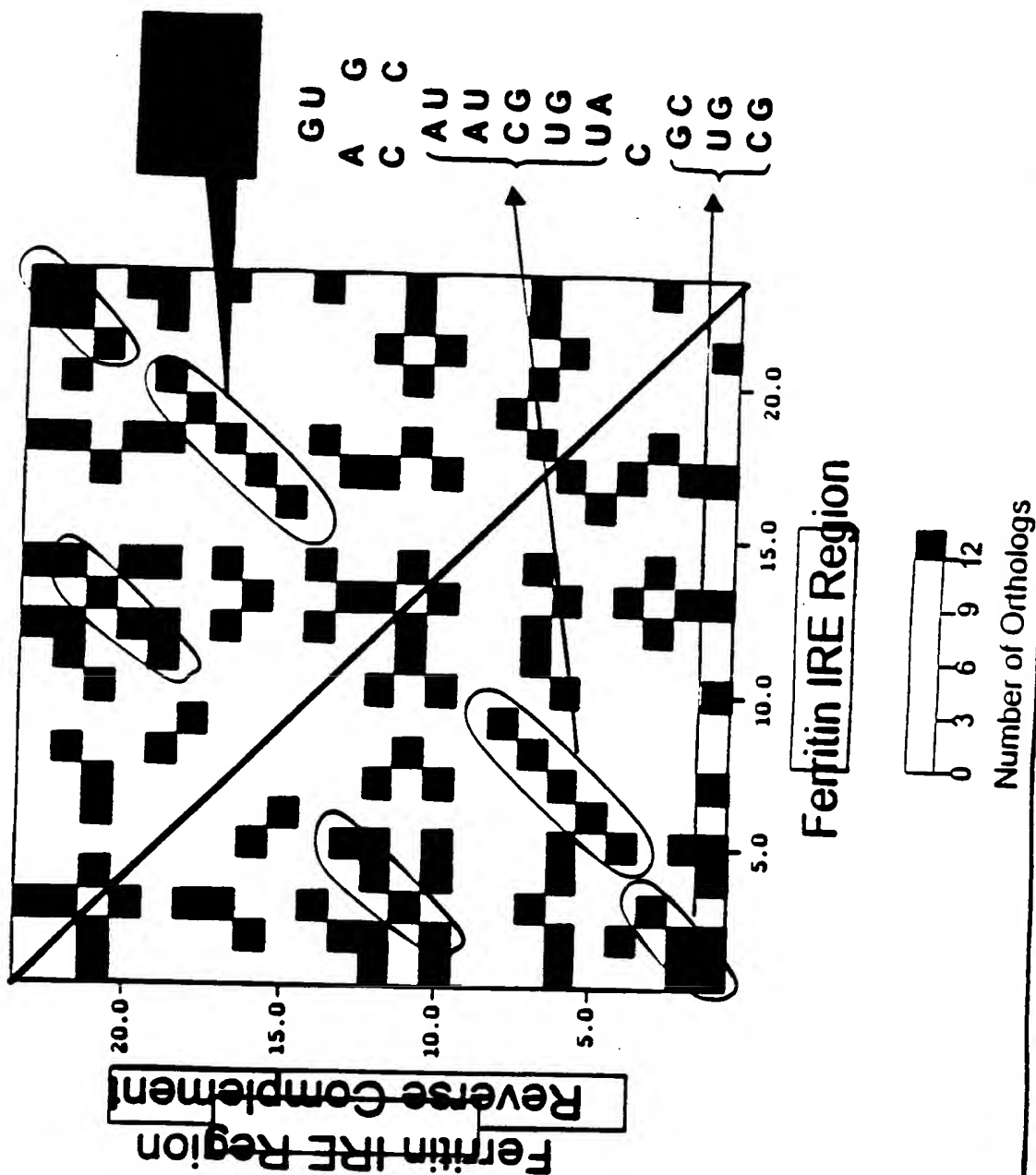
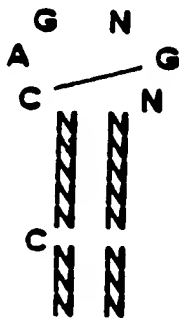


FIGURE 8

## Typical Descriptor

This is an example of a descriptor used to identify iron response elements. To search the database using RNAMOT, the stem-loop model is converted to a text string as shown below:



IRE

Stem-loop  
Model

H1 S1 H2 S2 H2 H1

H1 3:3 NNN:NNN

S1 1 C

H2 5:5 NNNNN:NNNNN

S2 6 CAGNGN

W2

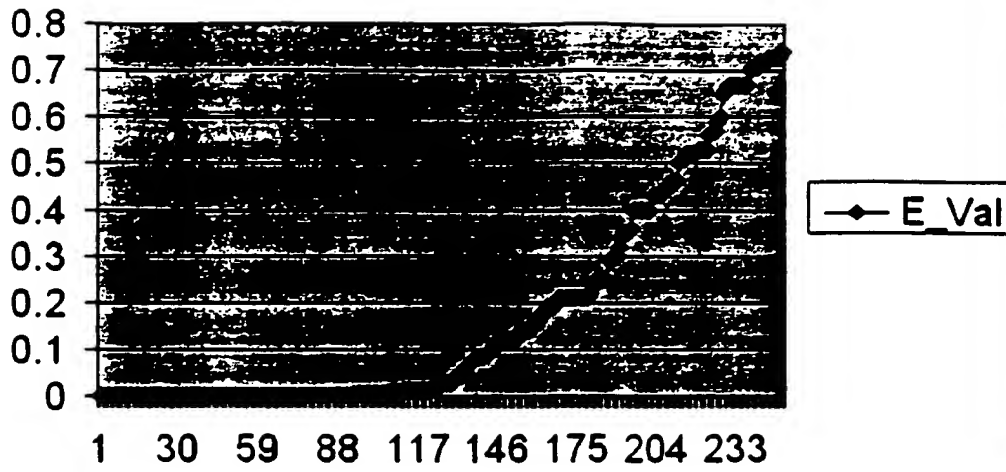
M0

IRE String descriptor

This descriptor allows for a wobble (W) of 2 (allows G-U pairing) and no mismatches. N can be any nucleotide. H refers to the stem region while S refers to the single stranded region.

FIGURE 9

E\_Val



00310667 051299  
662750 29907E60

FIGURE 10

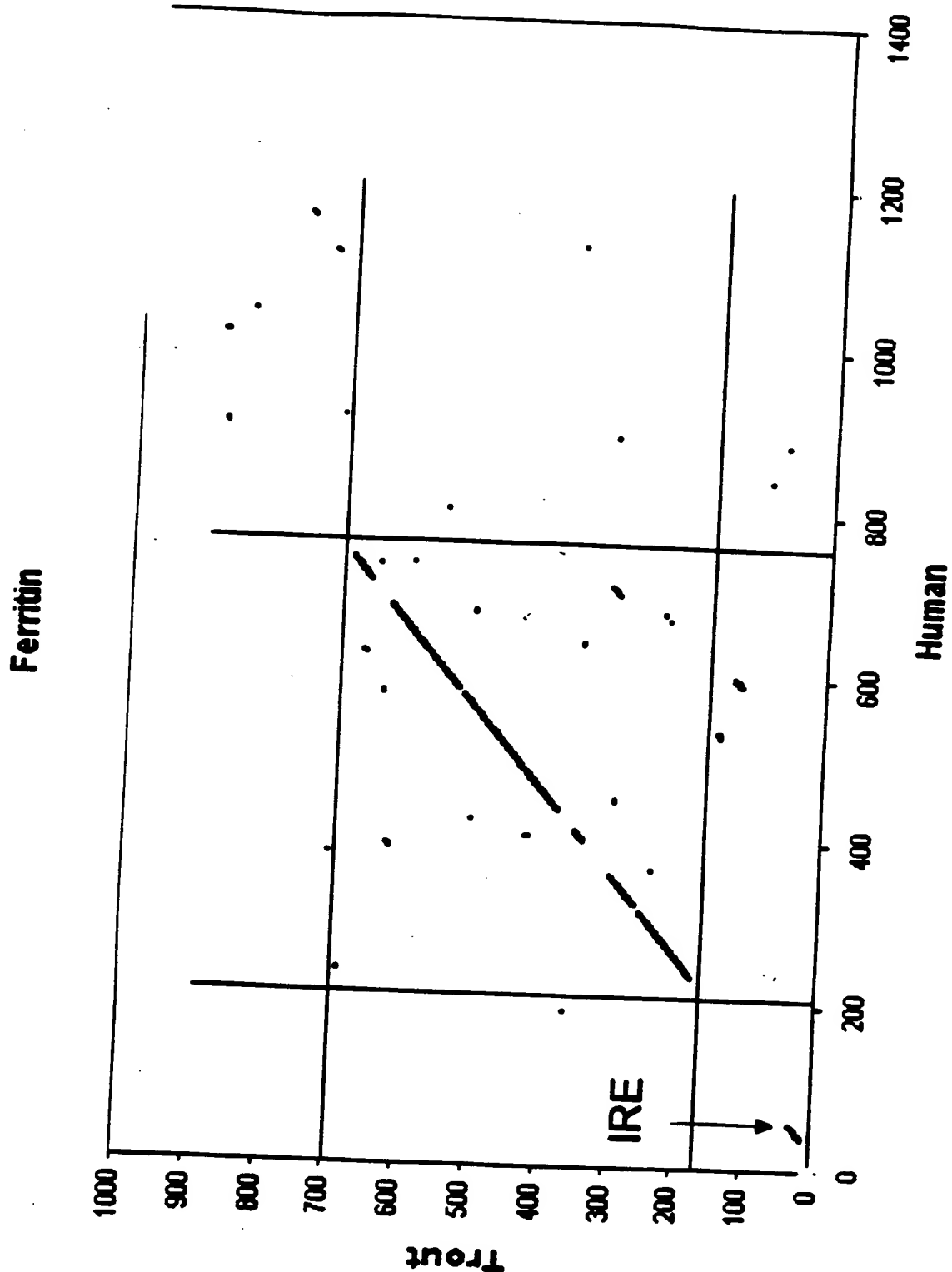


FIGURE 11

662T50-2990TE60

Ferritin

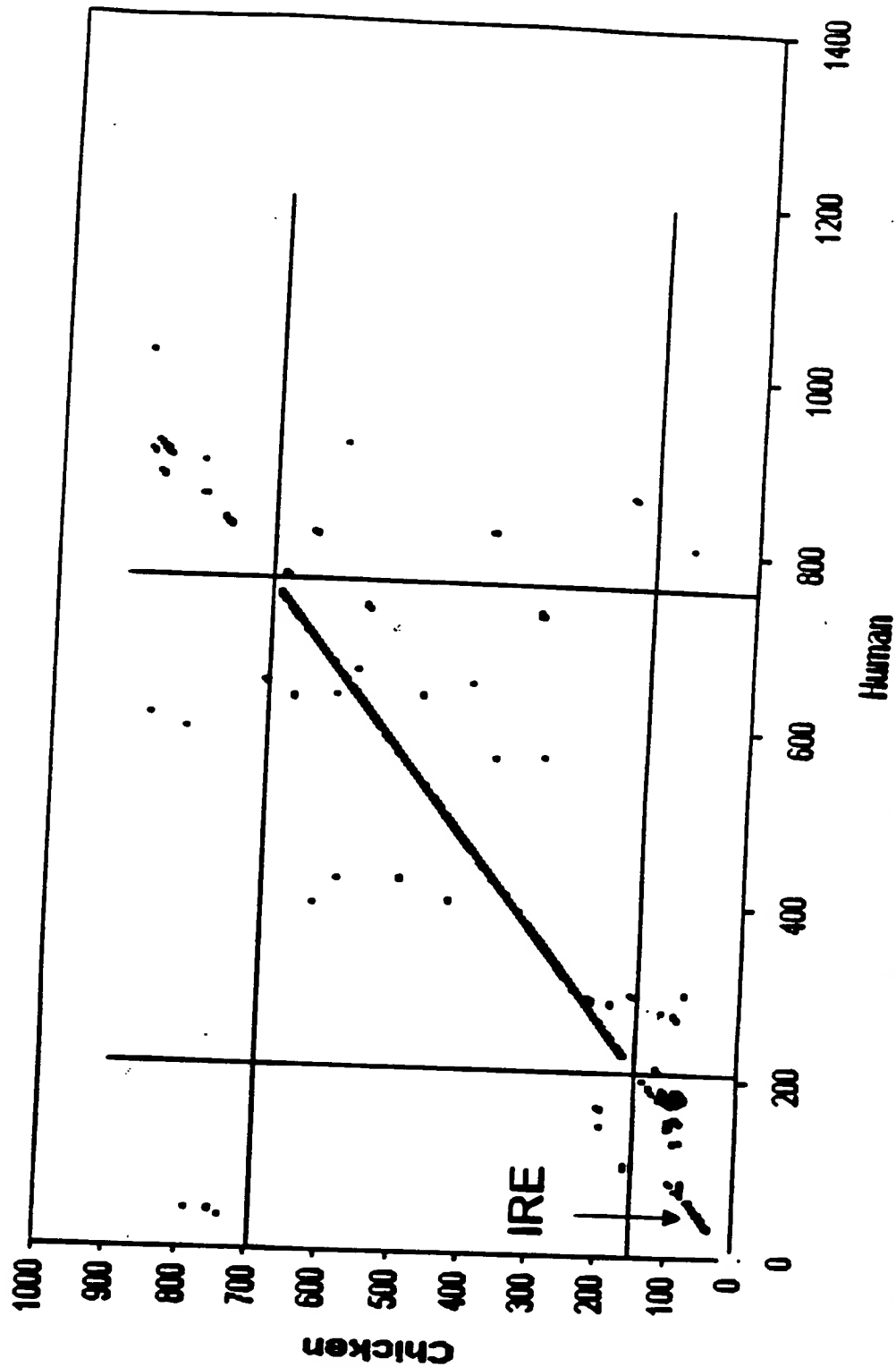


FIGURE 12

G-U A G G G U  
 C C C C C U  
 A-U A-U C-G U-G U-A C  
 G-C U-G C-G  
 HUMAN PIG

G-U A G G G U  
 C C C C C U  
 A-U A-U C-G U-G U-A C  
 G-C U-G C-G  
 HAMSTER MOUSE

G-U A G G G U  
 C C C C C U  
 A-U A-U C-G U-G U-A C  
 G-C U-G C-G  
 CHICKEN

G-U A G G G U  
 C C C C C U  
 A-U A-U C-G U-G U-A C  
 G-C U-G C-G  
 TROUT SALMON

G-U A G G G U  
 C C C C C U  
 A-U A-U C-G U-G U-A C  
 G-C U-G C-G  
 XENOPUS FROG

G-U A G G G U  
 C C C C C U  
 A-U A-U C-G U-G U-A C  
 G-C U-G C-G  
 FLY

G-U A G G G U  
 C C C C C U  
 A-U A-U C-G U-G U-A C  
 G-C U-G C-G  
 MOSQUITO

HUMAN PIG	HAMSTER MOUSE RAT	CHICKEN	TROUT SALMON	XENOPUS FROG	FLY	MOSQUITO
No	No	Yes	Yes	Yes	No	No
	No	Yes	Yes	Yes	No	No
		No	Yes	Yes	No	No
			No	Yes	Yes	Yes
				No	Yes	Yes
					No	Yes
						No

FIGURE 13



Figure 14

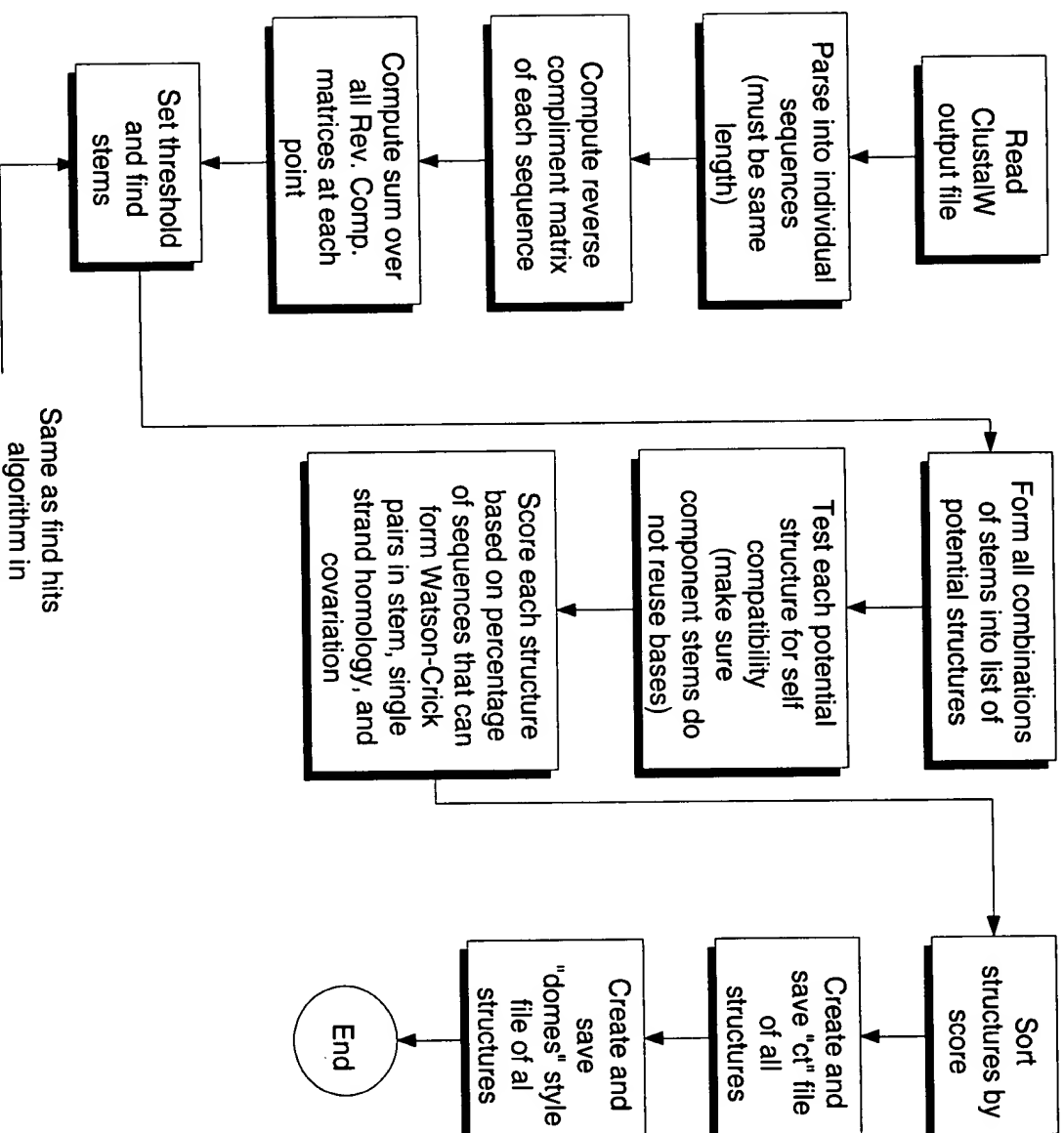
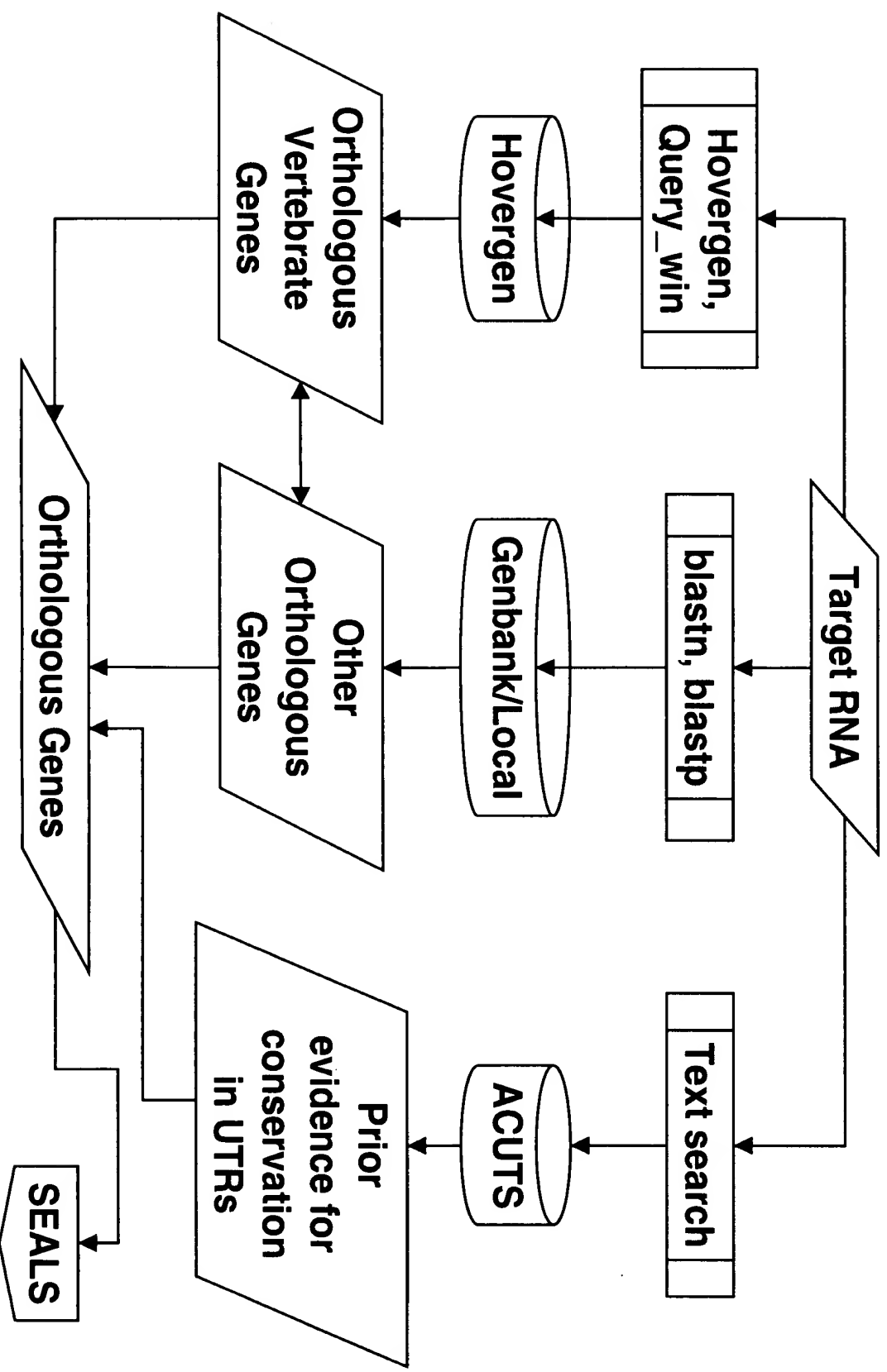


Figure 15



ferritin H subunit



**HOVERGEN**  
*Homologous Vertebrate Gene Data Base*

**Warning:** Phylogenetic trees are unrooted!  
 Select a gene or node (N) as outgroup to position the root (option= "New outgroup")

Get info

Select for Alignment

Select for Output

New outgroup

Swap nodes

Sub - tree

Reset tree

tree display ...

miscellaneous ...

☐ Small leaf

☐ Branch lengths

tree display ...

miscellaneous ...

☐ Small leaf

☐ Branch lengths

**Legend for Taxon Color**

Hovergen color file :

hovergen\_color

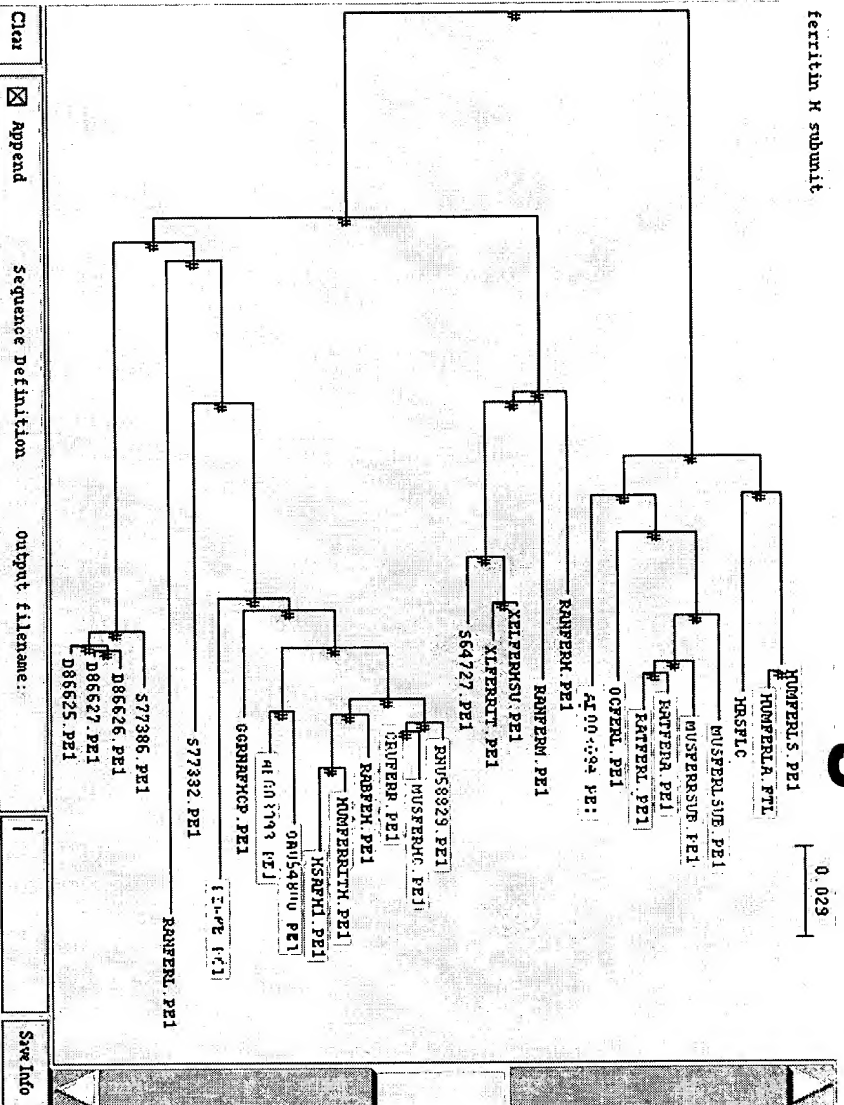
Change Color Set

<input type="checkbox"/>	HOMO SAPIENS
<input type="checkbox"/>	MUS MUSCULUS
<input type="checkbox"/>	RATTUS NORVEGICUS
<input type="checkbox"/>	GALLUS GALLUS
<input type="checkbox"/>	BOSTAUREUS
<input type="checkbox"/>	XENOPUS LAEVIS
<input type="checkbox"/>	ORYCTOLAGUS CUNICULUS
<input type="checkbox"/>	SUS SCROFA
<input type="checkbox"/>	CAVIA PORCELLUS
<input type="checkbox"/>	DANIO RERIO
<input type="checkbox"/>	OVIS ARIES
<input type="checkbox"/>	MAMMALIA
<input type="checkbox"/>	Other

**species**

Apply

# Figure 17



09310667 051299

**HOMOTEN**

*homotenus Vertebrate Genes Data Base*

---

**Warning:** Phylogenetic trees are unrooted!  
Select a gene or node (#) as outgroup to position the root. (option= "New outgroup")

Get info	Small leaf
Select for Alignment	<input type="checkbox"/> Branch lengths
Select for Output	
New outgroup	
Swap nodes	
Sub - tree	
Reset tree	

tree display ...	miscellaneous ...	<input type="button" value="◀"/> <input type="button" value="New Tree"/> <input type="button" value="▶"/>
------------------	-------------------	---

**Figure 18**

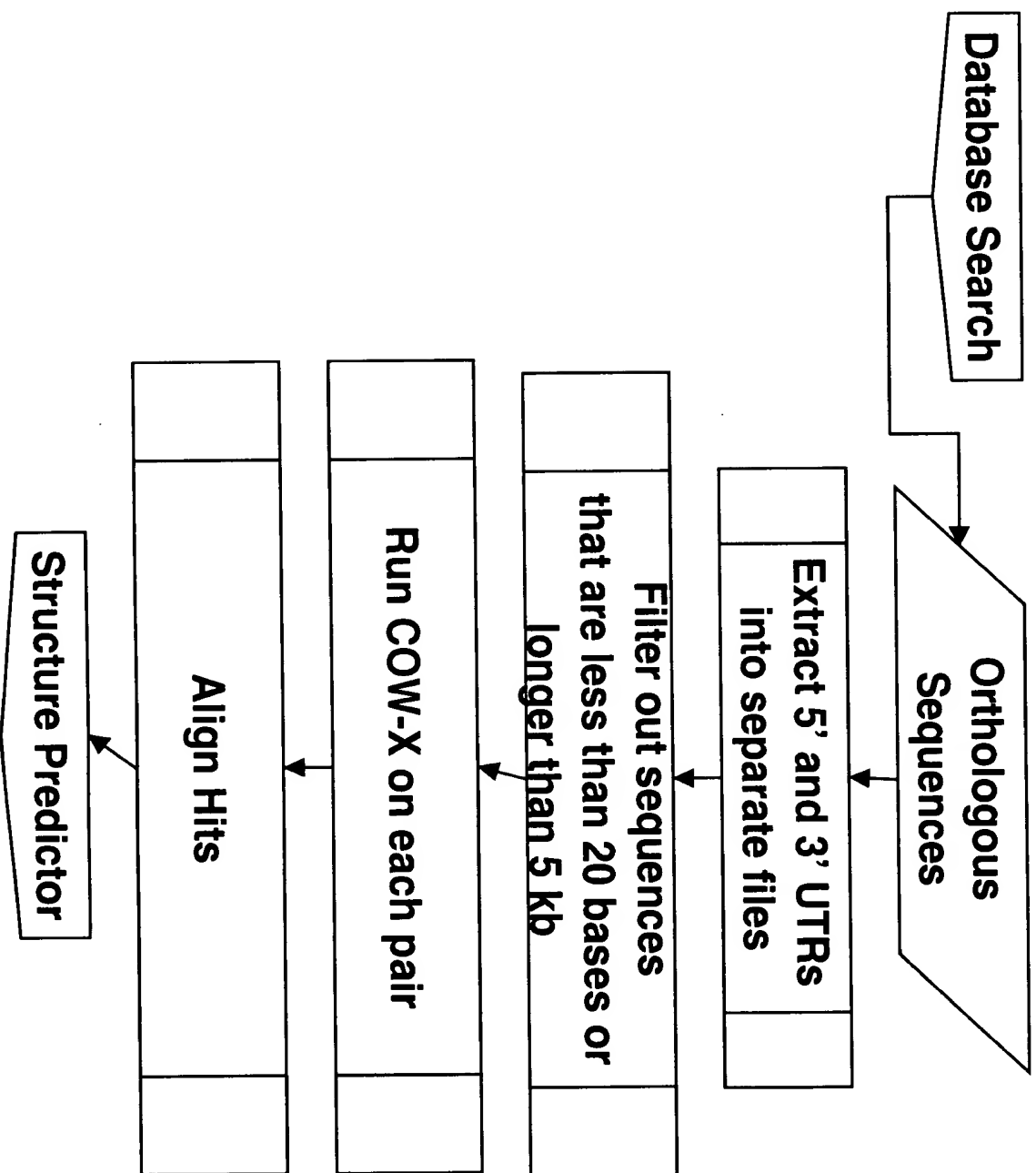


Figure 19

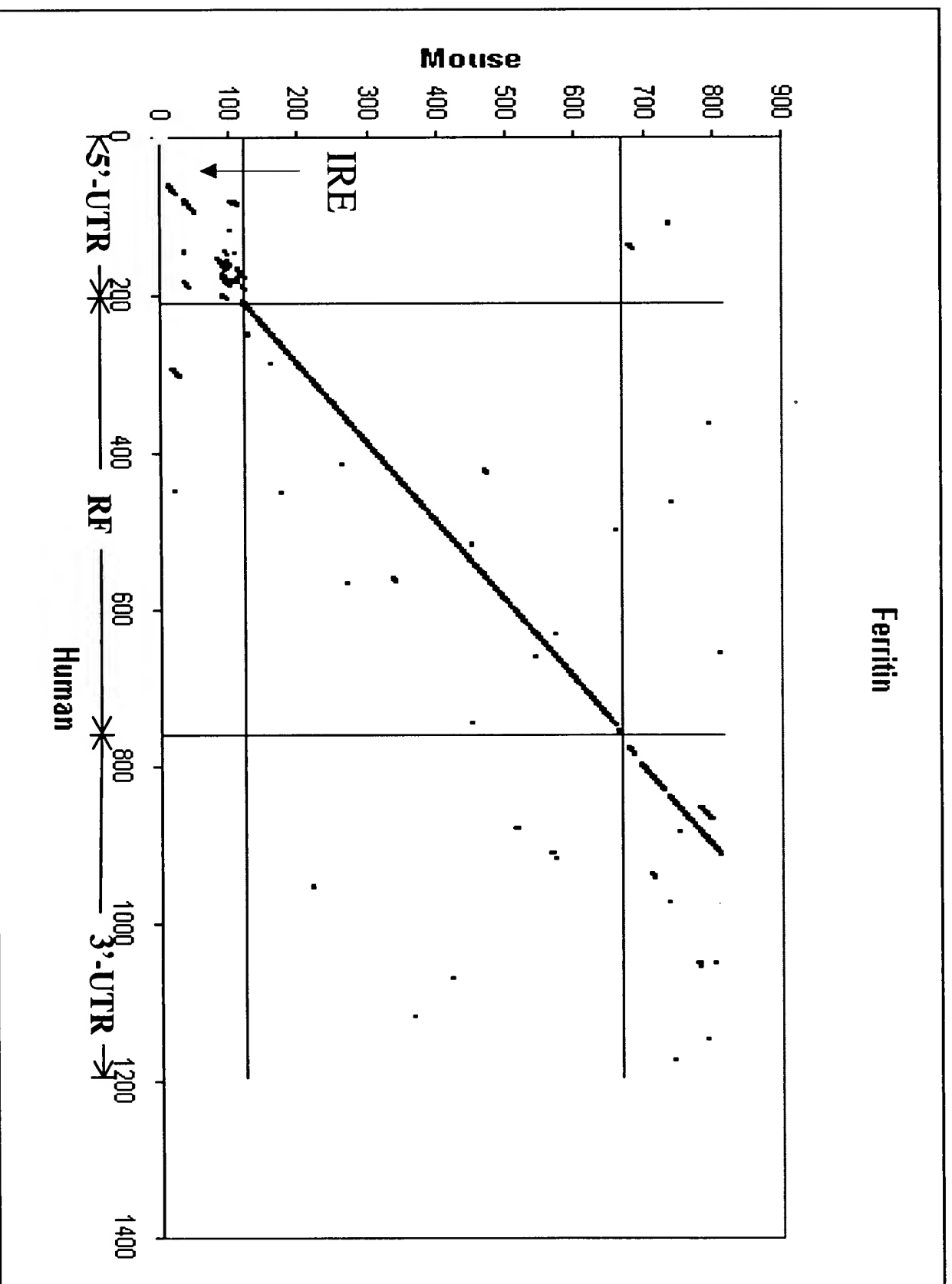


Figure 20

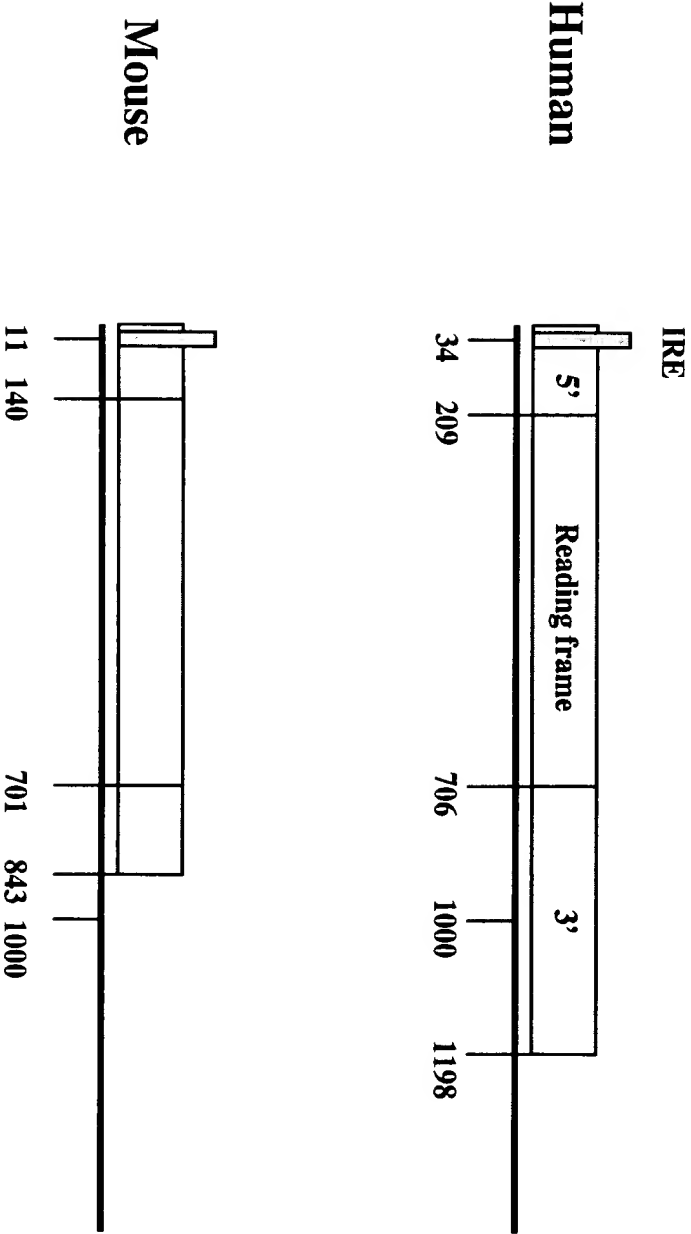


Figure 21

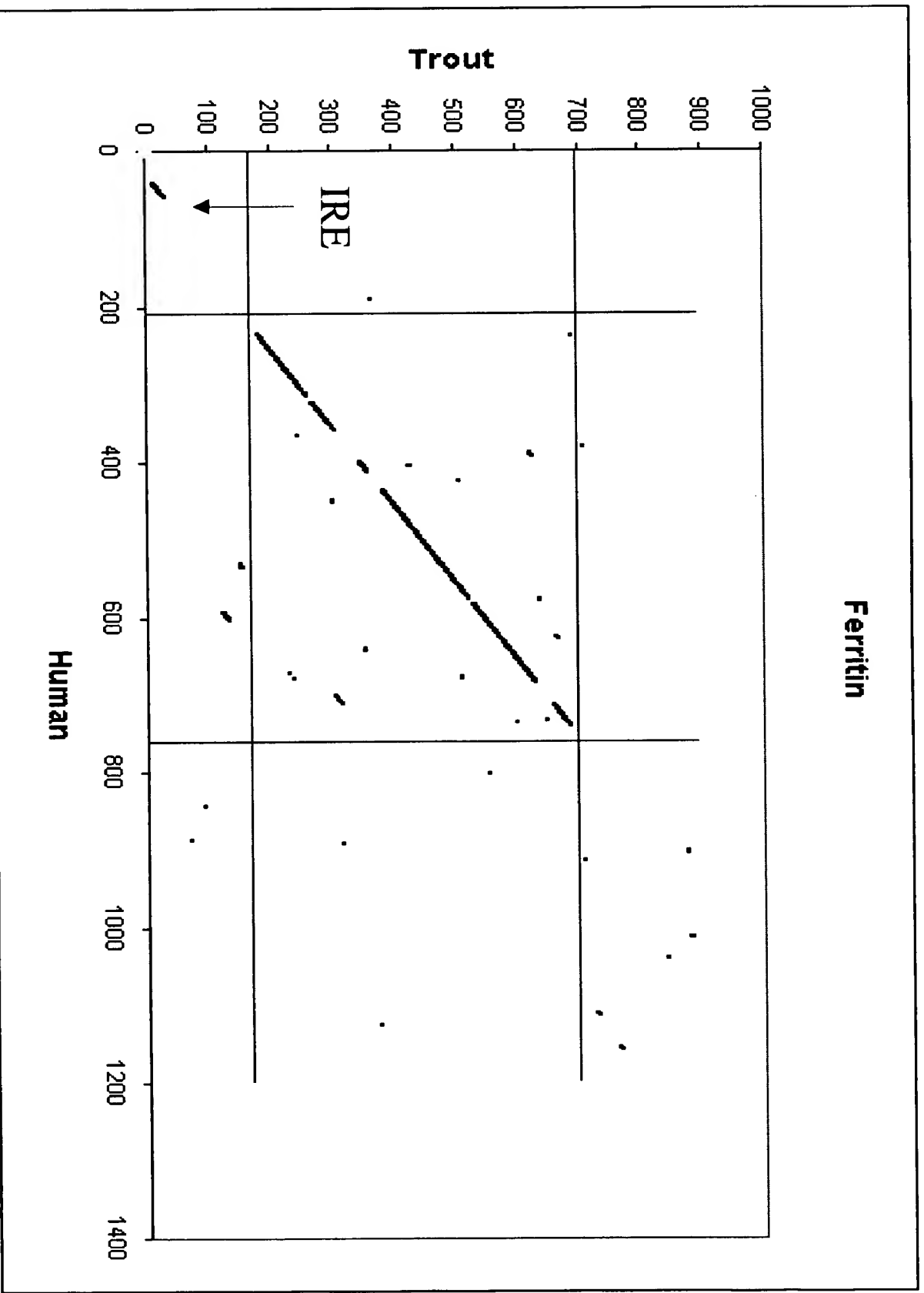




Figure 22

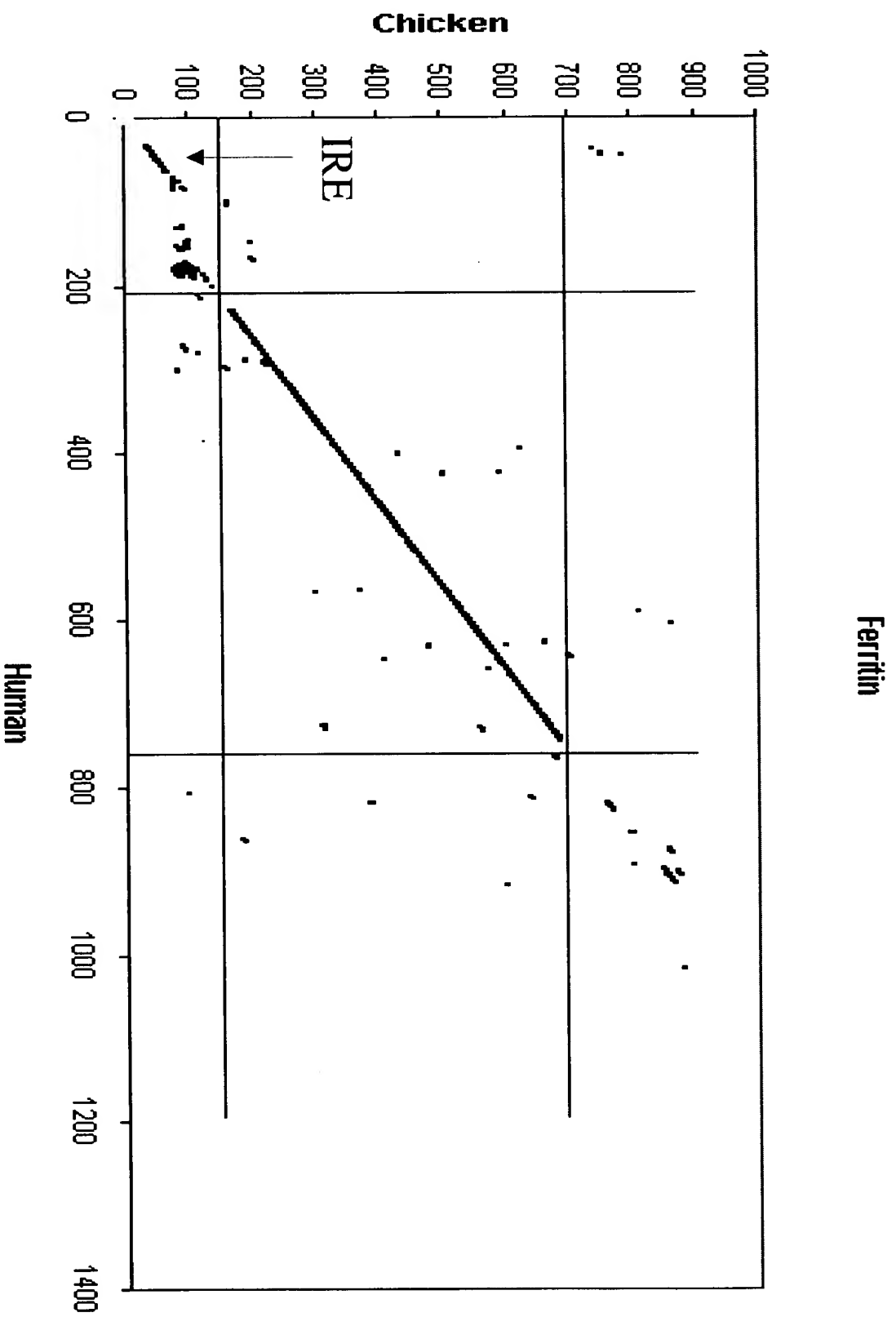
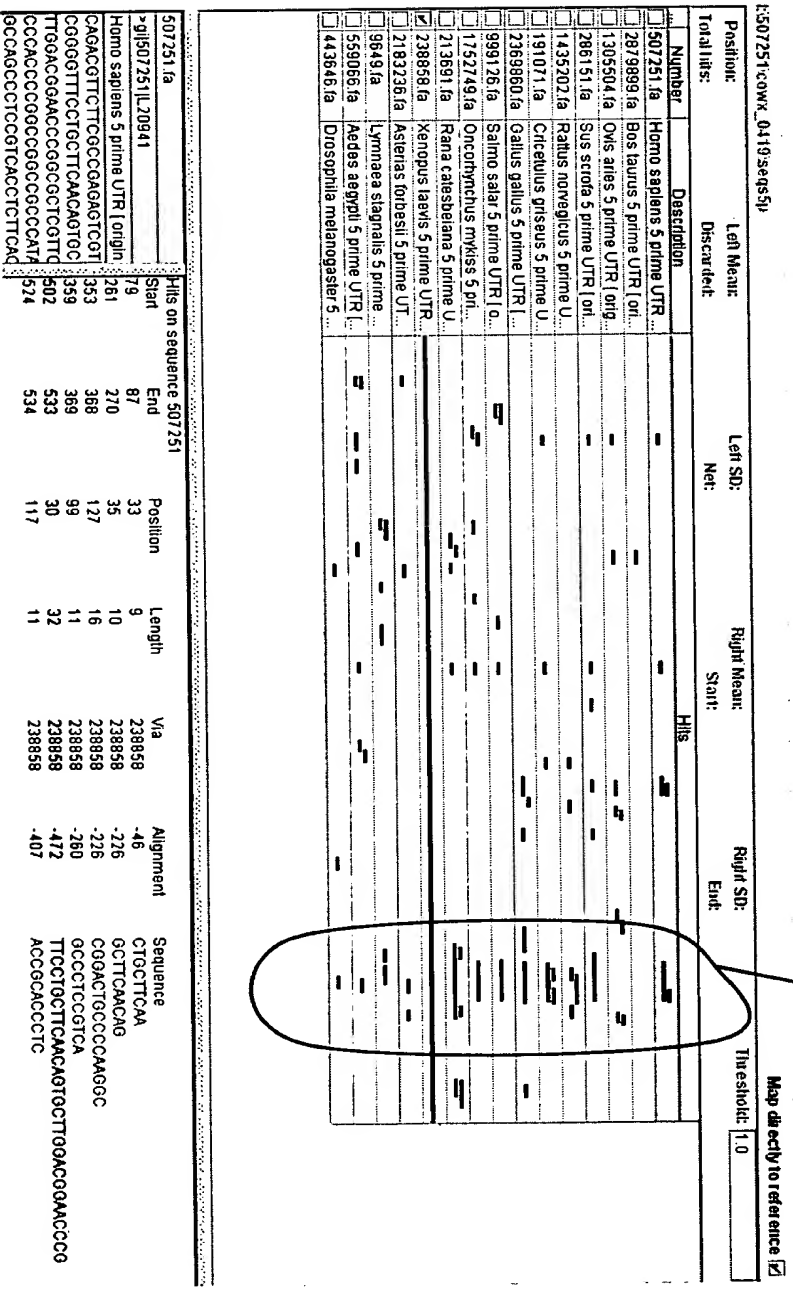


Figure 23

Conserved Region



09310657 051249

# Figure 24

5p_xenopus_500_535_auto.aln [Read-Only]		A	
1	CLUSTAL W (1.74) multiple sequence alignment		
2			
3			
4	gi 1752749 D86626	AGAACTTGCTTC AACAGTGATTG AACGGA ACTCCTC-	
5	gi 999126 S77386	AGTCTTGCTTC AACAGTGATTG AACGGA ACTCCTC-	
6	gi 213691 M12120	AGTCTTGCTTC AACAGTGTTG AACGGA AC-CCTCT	
7	gi 238858 S64727	AGTCTTGCTTC AACAGTGTTG AACGGA AC-CCTCT	
8	gi 286151 D15071	GTTTCCTGCTTC AACAGTGCTTG AACGGA ACCCGGC-	
9	gi 507251 L20941	GTTTCCTGCTTC AACAGTGCTTG AACGGA ACCCGGC-	
10	gi 191071 M99692	GTTTCCTGCTTC AACAGTGCTTG AACGGA ACCCGGC-	
11	gi 2369860 Y14698	GGTTCCTGCGTC AACAGTGCTTG AACGGA ACCCGGC-	
12	*** ***** *		
13			
14			
15			

Figure 25

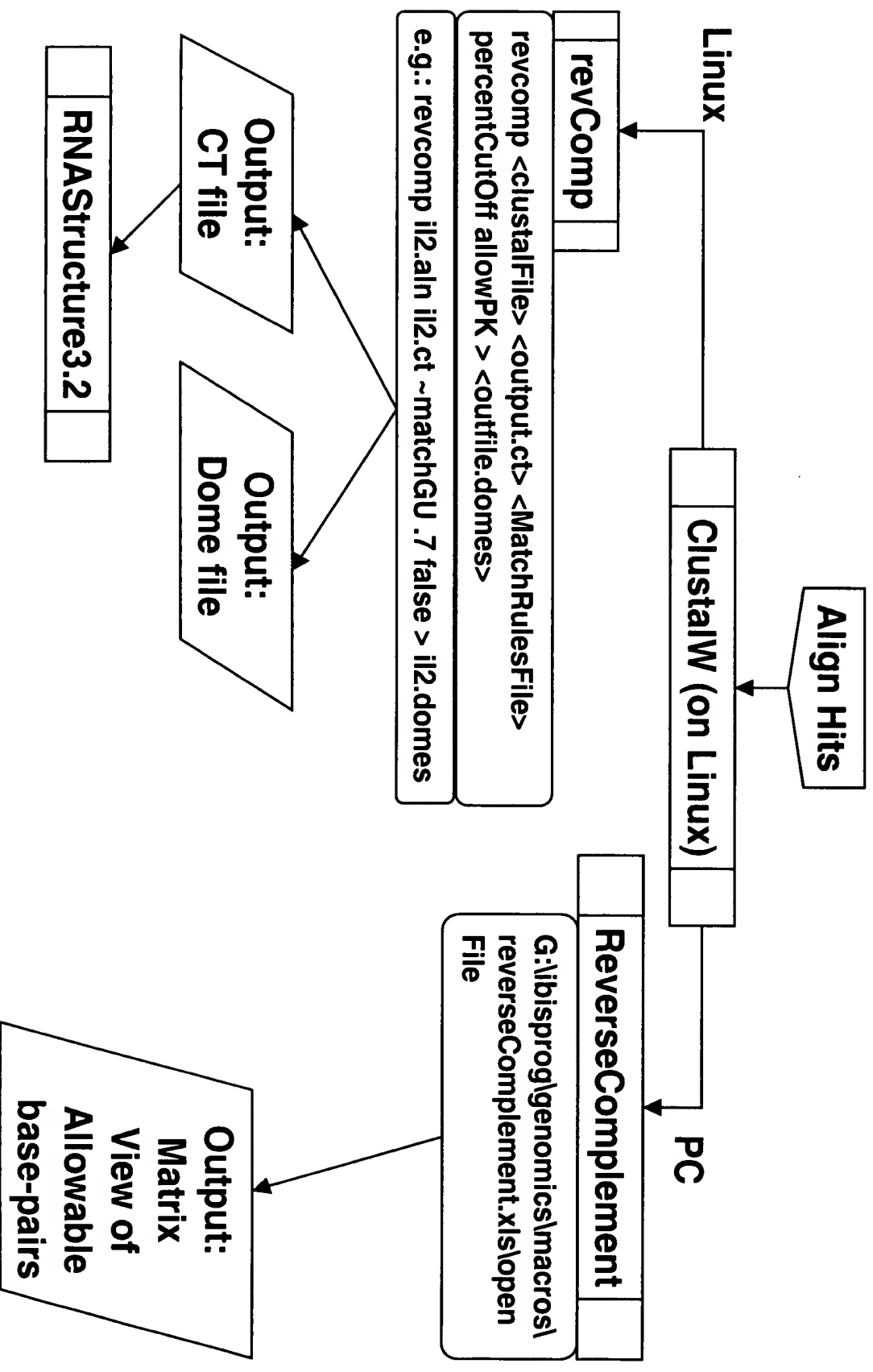
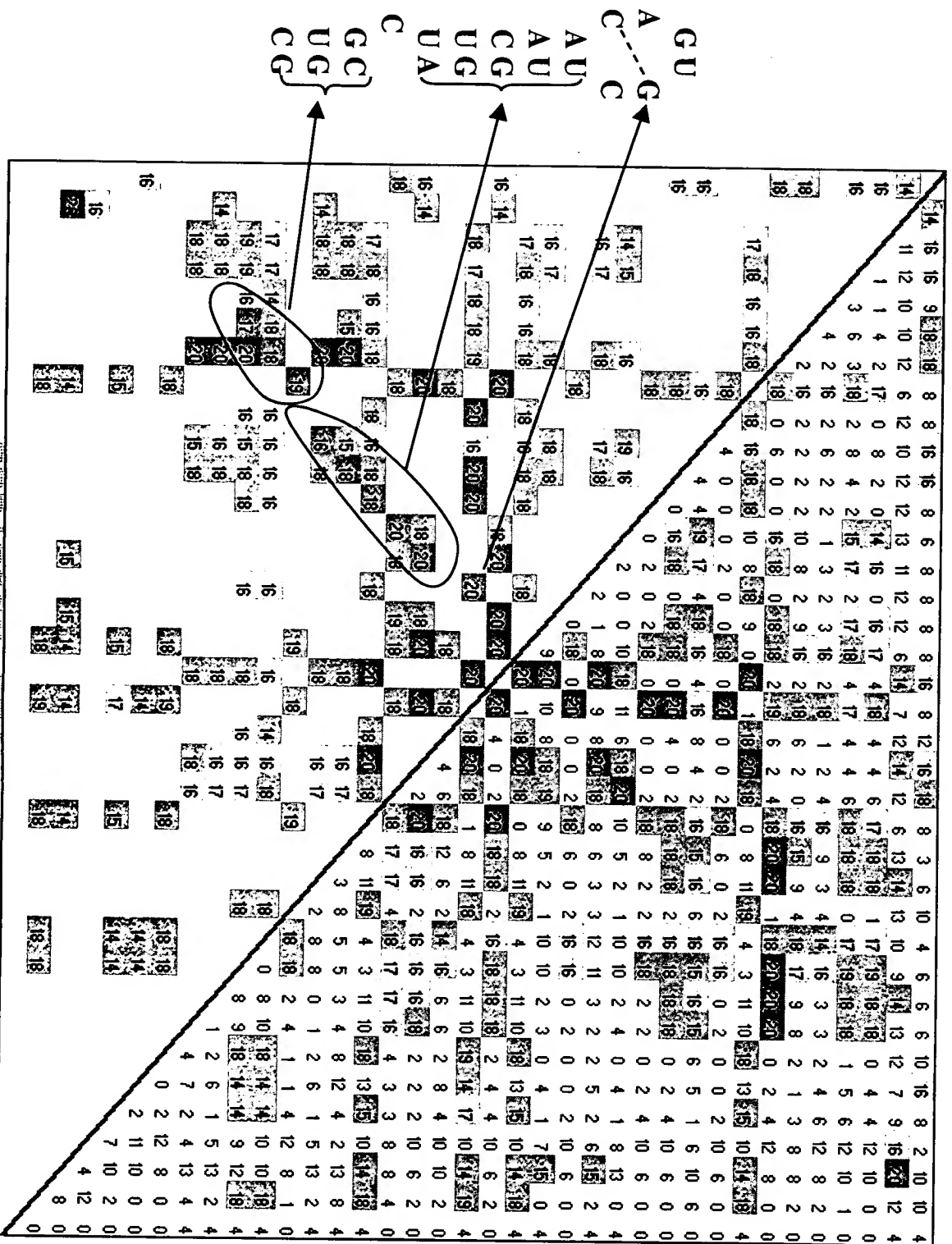
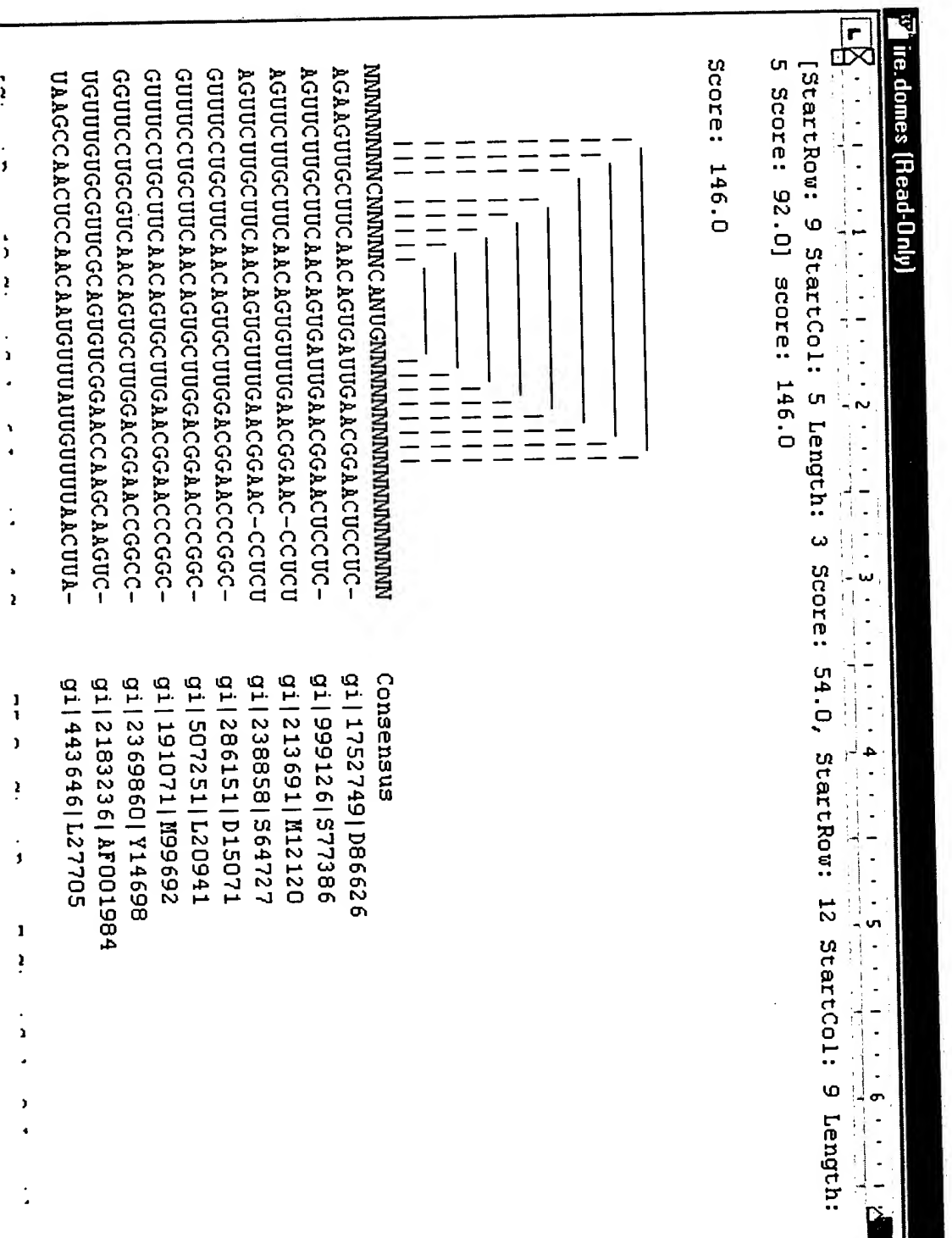


Figure 26



09310657-051299

Figure 27



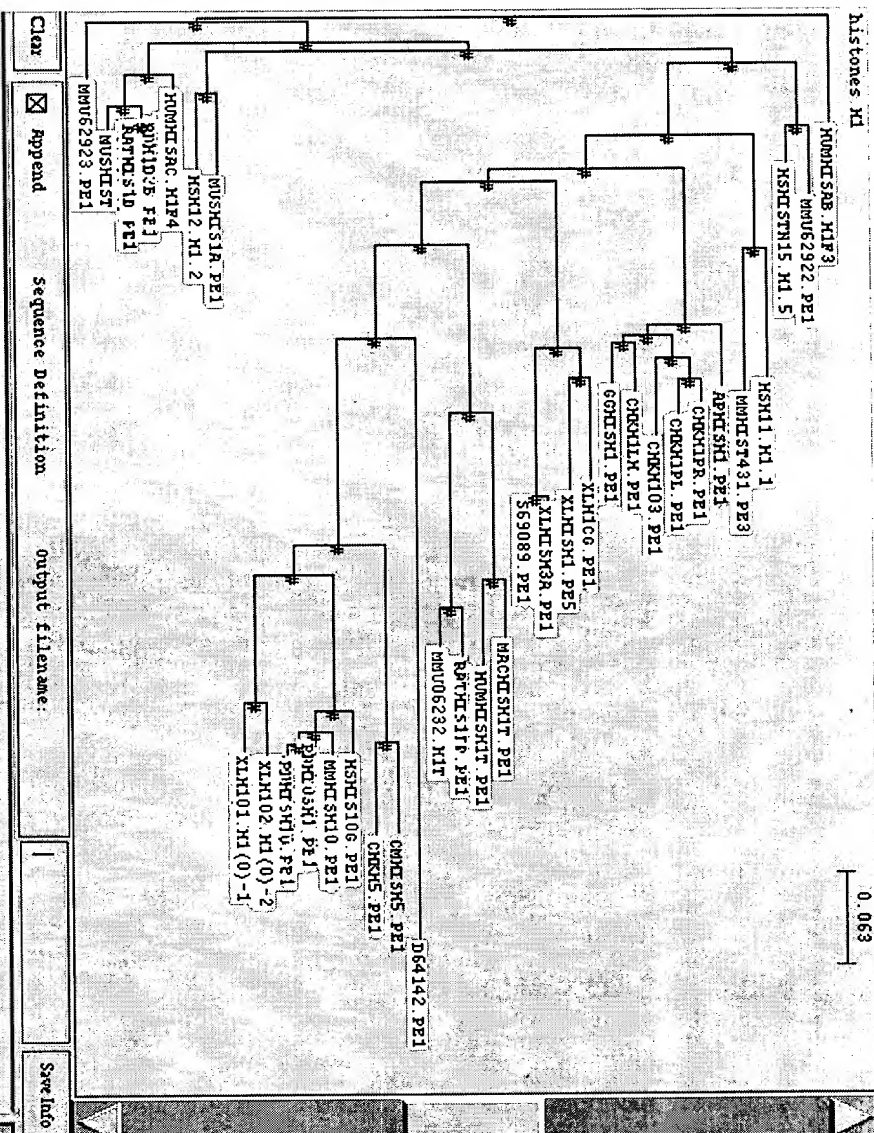
09310667.051299

Figure 28

IRE Structures for each species

	<div><div>G-U</div><div>A G</div><div>C C</div></div>	<div><div>G-U</div><div>A G</div><div>C C</div></div>	<div><div>G-U</div><div>A G</div><div>C C</div></div>	<div><div>G-U</div><div>A G</div><div>C A</div></div>	<div><div>G-U</div><div>A G</div><div>C U</div></div>	<div><div>G U</div><div>A G</div><div>C U</div></div>	<div><div>G U</div><div>A G</div><div>C U</div></div>
	<div><div>A-U</div><div>A-U</div><div>C-G</div><div>U-G</div><div>U-A</div></div>	<div><div>A-U</div><div>A-U</div><div>C-G</div><div>U-A</div><div>U-A</div></div>	<div><div>A-U</div><div>A-U</div><div>C-G</div><div>U-G</div><div>G-A</div></div>	<div><div>A-U</div><div>A-U</div><div>C-G</div><div>U-A</div><div>U-A</div></div>	<div><div>A-U</div><div>A-U</div><div>C-G</div><div>U-A</div><div>U-A</div></div>	<div><div>C-G</div><div>G-U</div><div>C-G</div><div>G-U</div><div>U-A</div></div>	<div><div>C-G</div><div>G-U</div><div>C-G</div><div>G-U</div><div>U-A</div></div>
HUMAN	<div><div>C</div><div>G-C</div><div>U-G</div><div>C-G</div></div>	<div><div>C</div><div>G-C</div><div>U-G</div><div>C-G</div></div>	<div><div>C</div><div>G-C</div><div>U-G</div><div>C-G</div></div>	<div><div>C</div><div>G-C</div><div>U-G</div><div>U-G</div></div>	<div><div>C</div><div>G-C</div><div>U-G</div><div>U-G</div></div>	<div><div>C</div><div>U-A</div><div>U-A</div><div>C-G</div></div>	<div><div>C</div><div>U-A</div><div>U-A</div><div>C-G</div></div>
PIG		<div><div>HAMSTER</div><div>MOUSE</div><div>RAT</div></div>	<div><div>CHICKEN</div></div>	<div><div>TROUT</div><div>SALMON</div></div>	<div><div>XENOPUS</div><div>FROG</div></div>	<div><div>FLY</div></div>	<div><div>MOSQUITO</div></div>

# Figure 29



09310667.051299

**HOVERGEN**  
Homologous Vertebrate Genes Data Base

Warning: Phylogenic trees are unrooted!  
Select a gene or node (\*) as outgroup to position the root (option="New outgroup")

☒ Get Info

☒ Selector for Alignment

☒ Selector for Output

☒ New outgroup

☒ Swap nodes

☒ Sub-tree

☒ Reset tree

☐ Small leaf

☐ Branch lengths

tree display ...

miscellaneous ...

New Tree

**Legend for Taxon Color**

Hovergen color file:

Change Color Set

HOMO SAPIENS

MUS MUSCULUS

RATTUS NORVEGICUS

GALLUS GALLUS

BOS TAURUS

XENOPUS LAEVIS

ORYZOLAGUS CUNICULUS

SUS SCROFA

CAVIA PORCELLUS

DANIO RERIO

OVIS ARIES

MAMMALIA

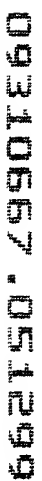
Other

species

Apply



### histones H1



**HOWERGEN**

*homologous Vertebrate Genes Data Base*

---

**Warning:** Phylogenetic trees are unrooted!  
Select a gene or node (#) as outgroup to position the root (option= "New outgroup")

<input checked="" type="checkbox"/> Get info <input checked="" type="checkbox"/> Select for Alignment <input checked="" type="checkbox"/> Select for Output <input checked="" type="checkbox"/> New outgroup <input checked="" type="checkbox"/> Swap nodes <input checked="" type="checkbox"/> Sub-tree <input checked="" type="checkbox"/> Root tree	<input type="checkbox"/> Small leaf  <input type="checkbox"/> Branch length
--	---

use display ...	miscellaneous ...	 New Tree 
-----------------	-------------------	------------------

Legend for Taxon Color      vertebrate classes      Apply

howergen color file :

Change Color Set

<input type="checkbox"/> MAMMALIA
<input type="checkbox"/> AVES
<input type="checkbox"/> SAUROPSIDA
<input type="checkbox"/> AMPHIBIA
<input type="checkbox"/> LOBE-FINNED FISH AND TETRAPOD CLADE
<input type="checkbox"/> ACTINOPTERYGII
<input type="checkbox"/> CHONDRICTHYEYES
<input type="checkbox"/> PETROMYZONTIFORMES
<input type="checkbox"/> MYXINIIFORMES
<input type="checkbox"/> Other

# Figure 31

Conserved Region

E:\HISTONE\cowx\_0416\seqs3p

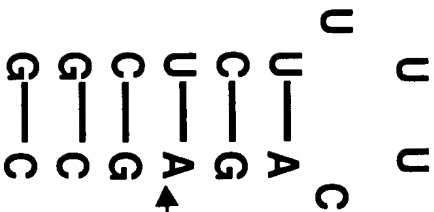
Position:		Left/Meant:		Left/SD:	
Total hits:		Discarded:		Net:	
...	Number	Description	Hits		
<input type="checkbox"/>	63477.fa	Gallus gallus 3 prime UTR [ ...	—		
<input type="checkbox"/>	9788.fa	Pisaster brevispinus 3 prime...	—		
<input type="checkbox"/>	349586.fa	Volvox carteri 3 prime UTR [ ...	—		
<input type="checkbox"/>	10044.fa	Pisaster ochraceus 3 prime ...	—		
<input type="checkbox"/>	9989.fa	Pycnopodia helianthoides 3 ...	—		
<input checked="" type="checkbox"/>	161381.fa	Psammochinus miliaris 3 pr...	—		
<input type="checkbox"/>	9614.fa	Lytechinus pictus 3 prime U...	—		
<input type="checkbox"/>	31967.fa	Homo sapiens 3 prime UTR ...	—		
<input type="checkbox"/>	64766.fa	Xenopus laevis 3 prime UTR...	—		
<input type="checkbox"/>	404465.fa	Styela plicata 3 prime UTR [ ...	—		
<input type="checkbox"/>	342113.fa	Macaca mulatta 3 prime UT...	—		
<input type="checkbox"/>	797284.fa	Paracentrotus lividus 3 prim...	—		
<input type="checkbox"/>	287651.fa	Rattus norvegicus 3 prime U...	—		
<input type="checkbox"/>	2292939.fa	Mus musculus 3 prime UTR ...	—		
<input type="checkbox"/>	62730.fa	Cairina moschata 3 prime U...	—		
<input type="checkbox"/>	10251.fa	Strongylocentrotus purpuratu...	—		
<input type="checkbox"/>	62440.fa	Anas platyrhynchos 3 prime ...	—		
<input type="checkbox"/>	10338.fa	Solaster stimpsoni 3 prime ...	—		
<input type="checkbox"/>	515003.fa	Mus pahari 3 prime UTR [ ori...	—		

# Figure 32

3p\_xenopus\_23\_56\_autoaln [Read-Only]

A	
1	CLUSTAL W (1.74) multiple sequence alignment
2	
3	
4	gi 10044 X54113 -TAAACAAAACGGCTCTTTTCAGAGCCACCACCTTC-
5	gi 9788 X54112 -TAAACAAAACGGCTCTTTTCAGAGCCACCACCTTC-
6	gi 9989 X54114 -TAATCAAAAACGGCTCTTTTCAGAGCCACCACCTTC-
7	gi 10251 V01356 ATACACAAA-CGGCTCTTTTCAGAGCCACCACAAC-
8	gi 161381 M10558 ATACACAAA-CGGCTCTTTTCAGAGCCACCACAAC-
9	gi 9614 X00628 TAACCAAAA-CGGCTCTTTTCAGAGCCACCATAAC-
10	gi 404465 S64499 -GACACAAAACGGCTCTTTTCAGAGCCACCACA-ATCG
11	gi 31967 X57129 AAACCCA-AAAGGCTCTTTTCAGAGCCACCACCTGA-
12	gi 515003 X80327 -CCCCACAAAAGGCTCTTTTCAGAGCCACCACCTGC-
13	gi 2292939 Y12291 -CAATCCAAAAGGCTCTTTTCAGAGCCACCACCTCC-
14	gi 287651 X67320 -ACAACCCAAAAGGCTCTTTTCAGAGCCACCACCAAA-
15	gi 342113 M97756 -AGAACCCAAAAGGCTCTTTTAAGAGCCACCACCAT-
16	gi 63477 X01752 -GATATCCAAACGGCTCTTTTAAGAGCCACCACACAC-
17	gi 64766 X03017 -TATACCCAAAAGGCTCTTTTCAGAGCCACCACACCC-
18	gi 62440 X06128 -TAAACCCAAAAGGCTCTTTTAAGAGCCACCACCTT-
19	gi 62730 X14731 -TTAACCCAAAAGGCTCTTTTCAGAGCCACCACCACTT-
20	gi 10338 X54115 -CAAACCGAAGCGCCCTTTTAGGCCACTACACTTT-
21	* * * * *
22	NNNNNNNNANNNGGCNCCTTTTNNNNNNNNNNNNNNNN
23	
24	

3p\_xenopus\_23\_56\_auto.aln [Read-Only]



051205Z

Figure 34

histone.domes (Read-Only)

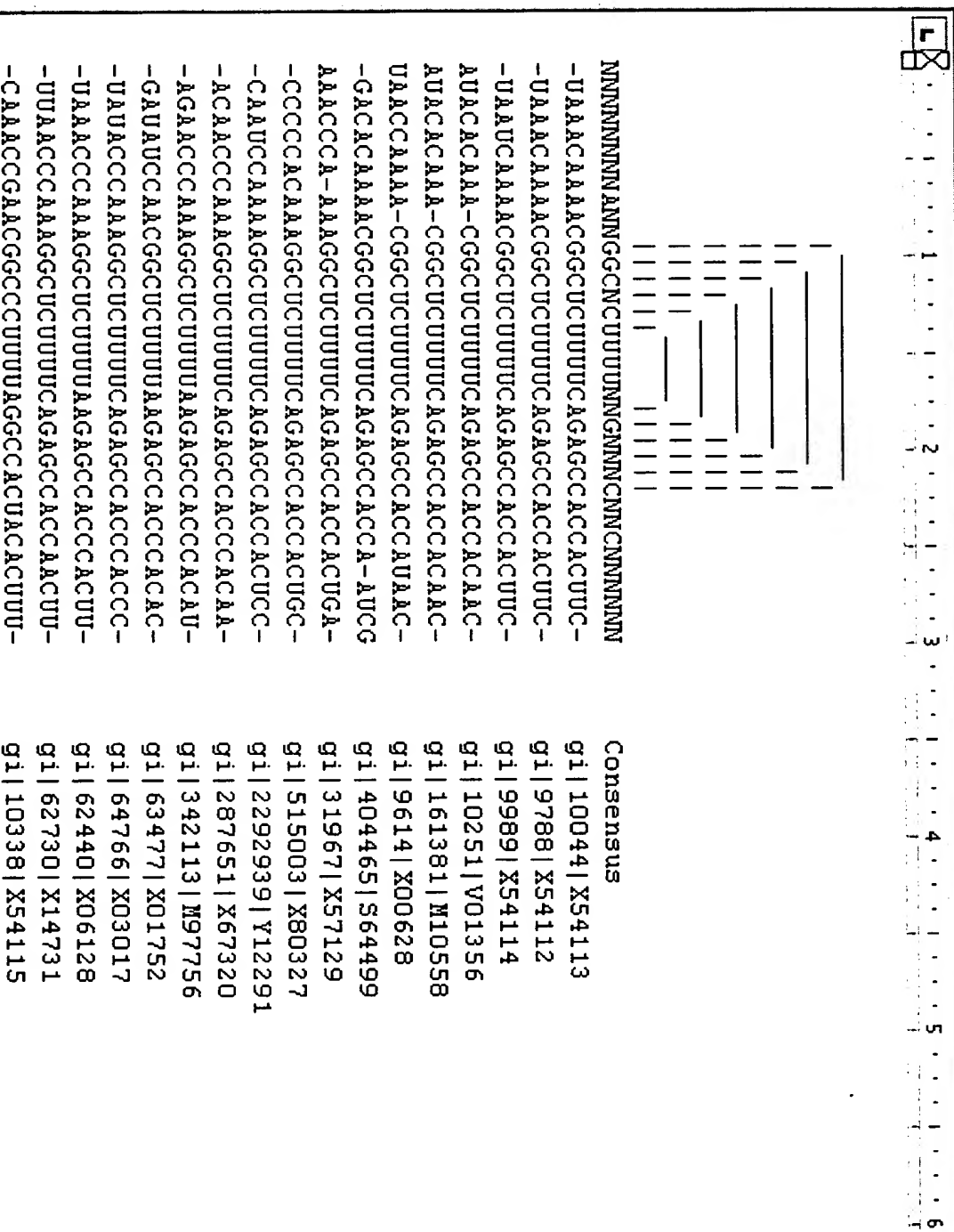


Figure 35

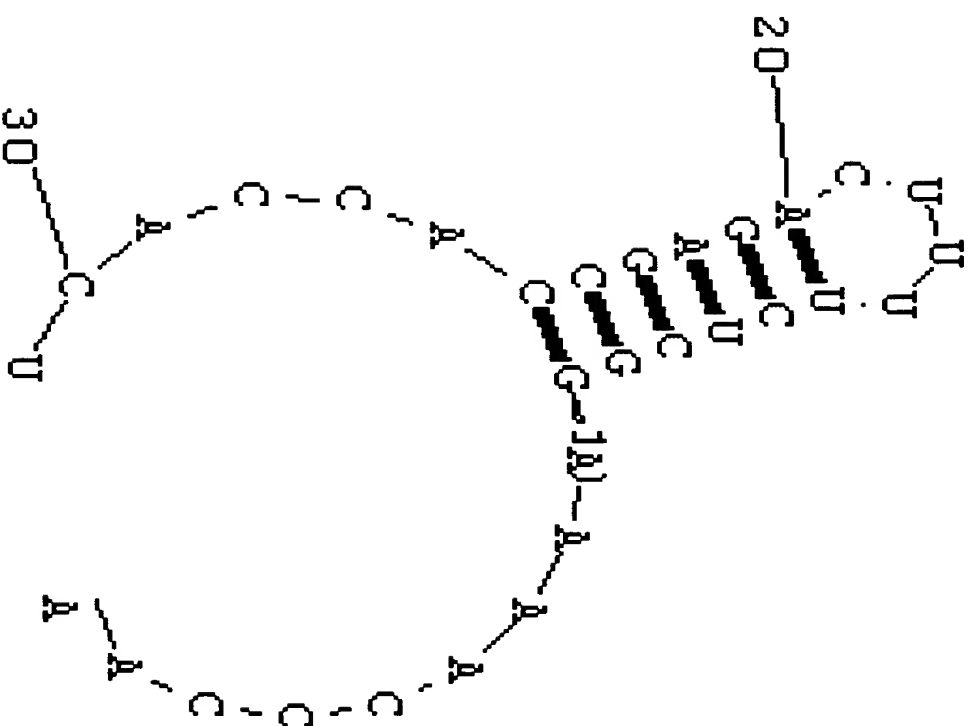


Figure 36

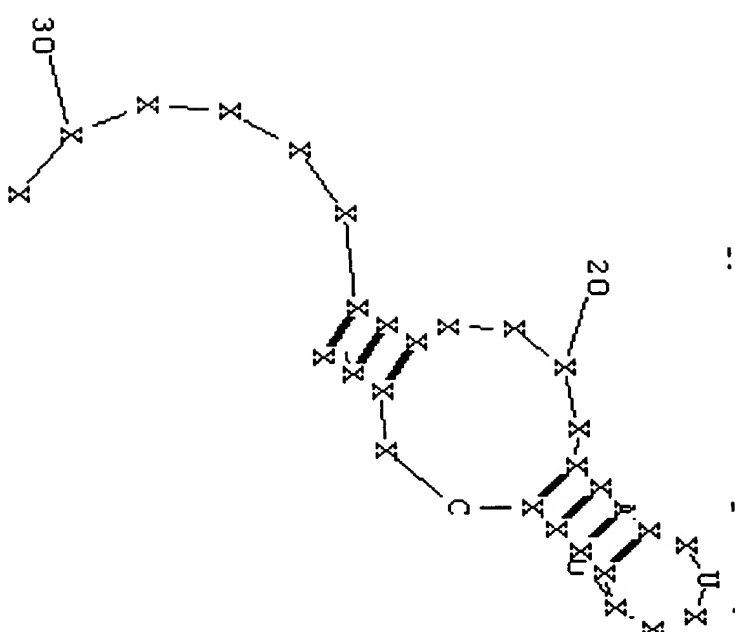
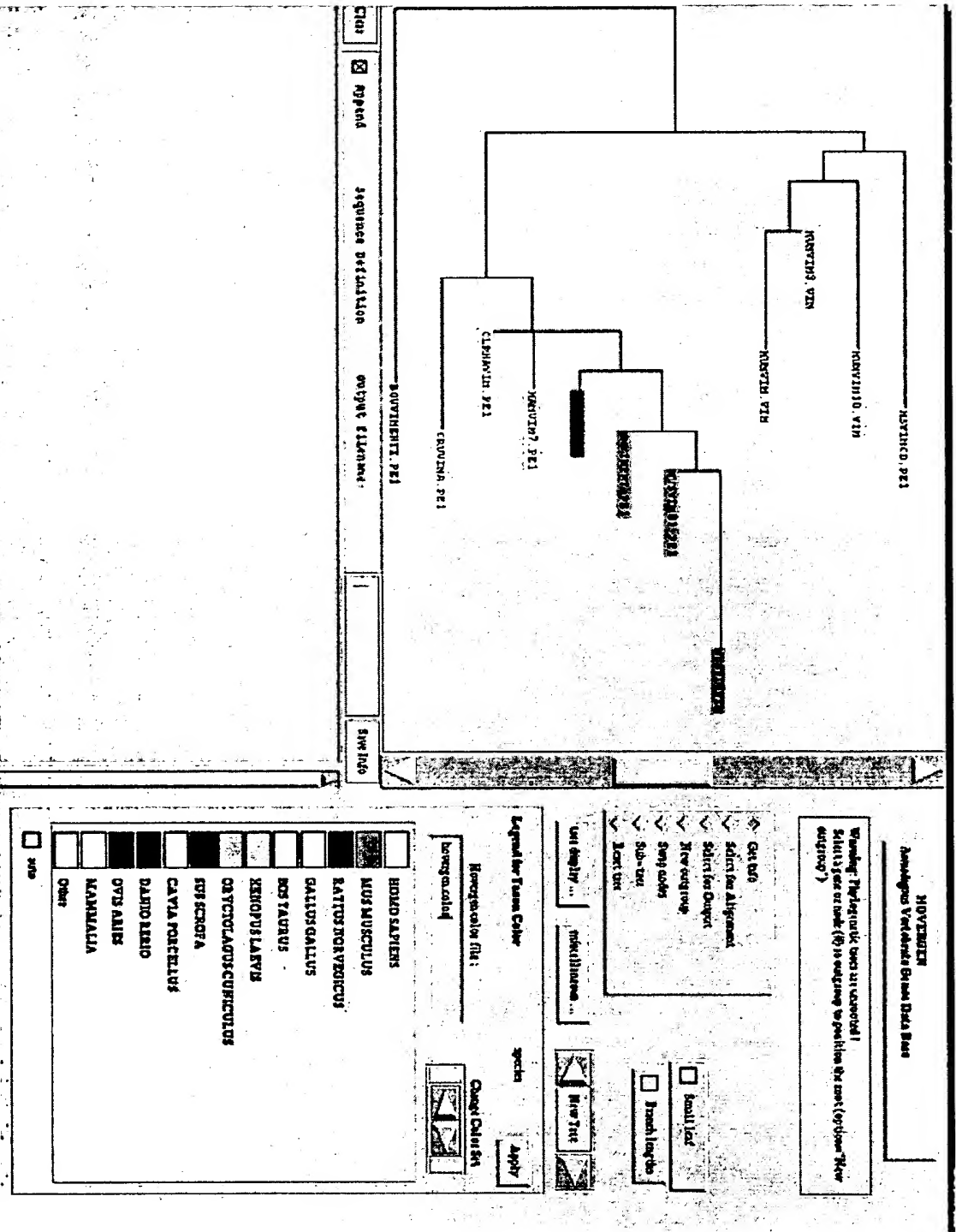


Figure 37



09310667.051299



Figure 38

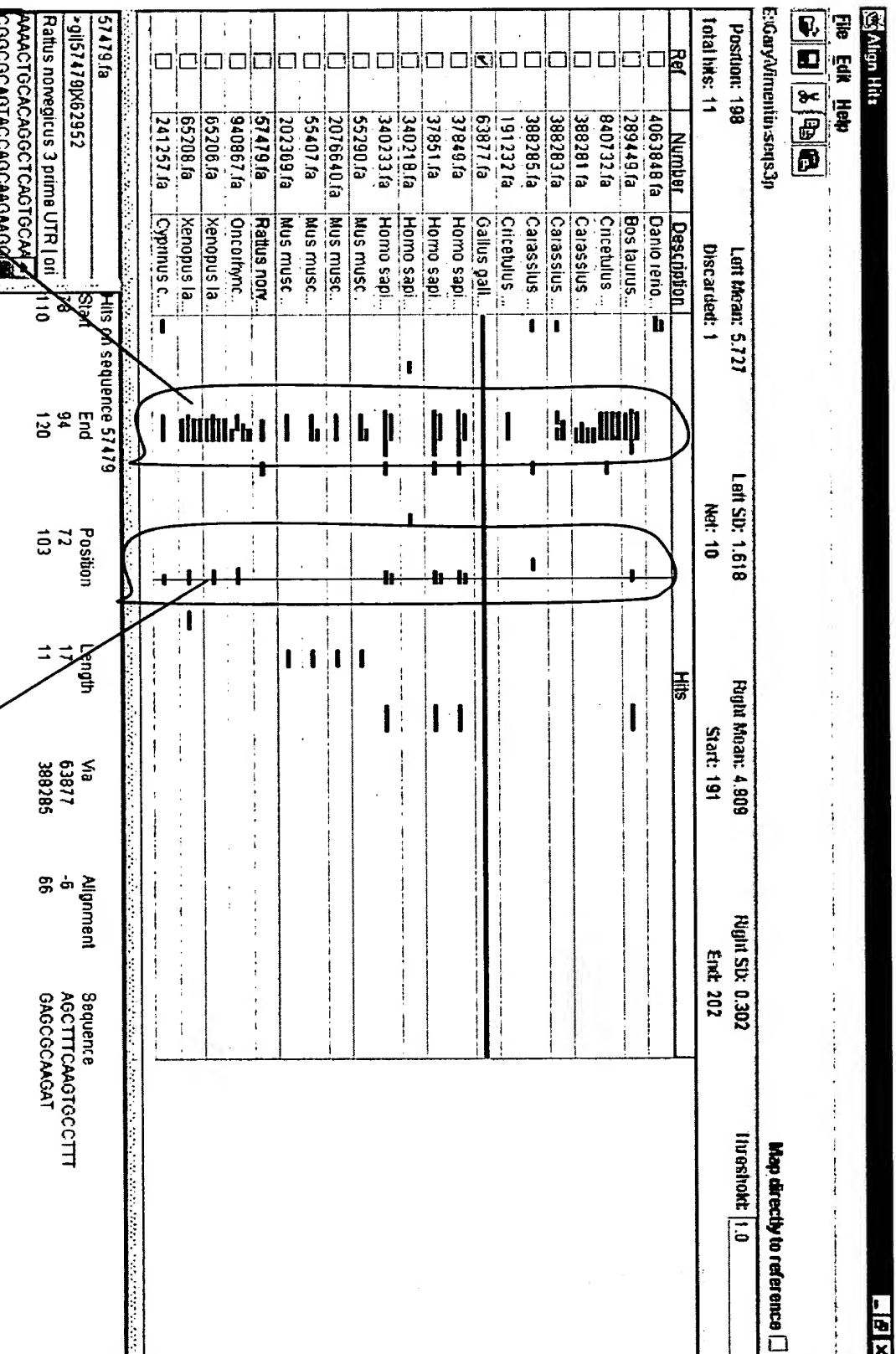


Figure 39

CLUSTAL W (1.74) multiple sequence alignment

```
gi|191232|M16718      TATCTTAAGGAAACAGCTTTTCAAGTGCCCTTCTGCAAGTTTTCAGAGCGCAAGTAA
gi|202369|M26251      TATCTTAGGAAAACAGCTTTCAAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
gi|2076640|Y07738     TATCTTAGGAAAACAGCTTTCAAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
gi|289449|L13263      TATCTTAAGAAACAGCTTTCAAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
gi|340233|M25246      TATCTTAAGAAACAGCTTTCAAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
gi|37849|X56134       TATCTTAAGAAACAGCTTTCAAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
gi|37851|Z19554       TATCTTAAGAAACAGCTTTCAAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
gi|388281|L23840      CAACCCACAATTAACGTGCTTCAAAAGTGCCCTTCTGCACAGAAATA--GCCTTGAGC
gi|388283|L23842      CTACCCACAATTAACGTGCTTCAAAAGTGCCCTTCTGC-CAGAAGTACAAGCATTTGAGC
gi|55290|X51438       TATCTTAGGAAAACAGCTTTCAAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
gi|55407|X56397       TATCTTAGGAAAACAGCTTTCAAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
gi|57479|X62952       TATCTTAGGAAAACAGCTTTCAAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
gi|63877|V00447       TGTCTTAAGGAAAGAGCTTTCAGAGTGCCCTTCTCCAGTTTTCATGAGCGCAAGATT
gi|65206|X16843       ACTTTGAAGAAAACAGCTTTCAGAGTGCCCTT-TGCAGTCAATGGAGAGCGCAAGATA
gi|65208|X16844       AATTTGAAGAAAACAGCTTTCAGAGTGCCCTT-TGCAGTTAATGGAGAGCGCAAGATA
gi|840732|X87227      TATCTTAAGGAAACAGCTTTCAGAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
```



Figure 41

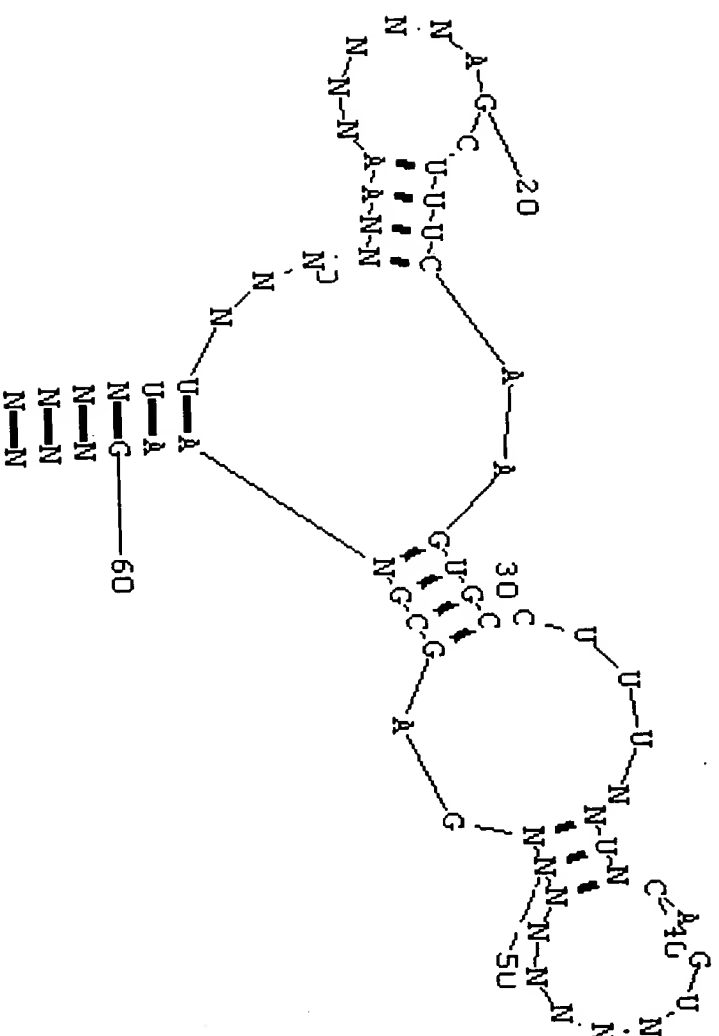
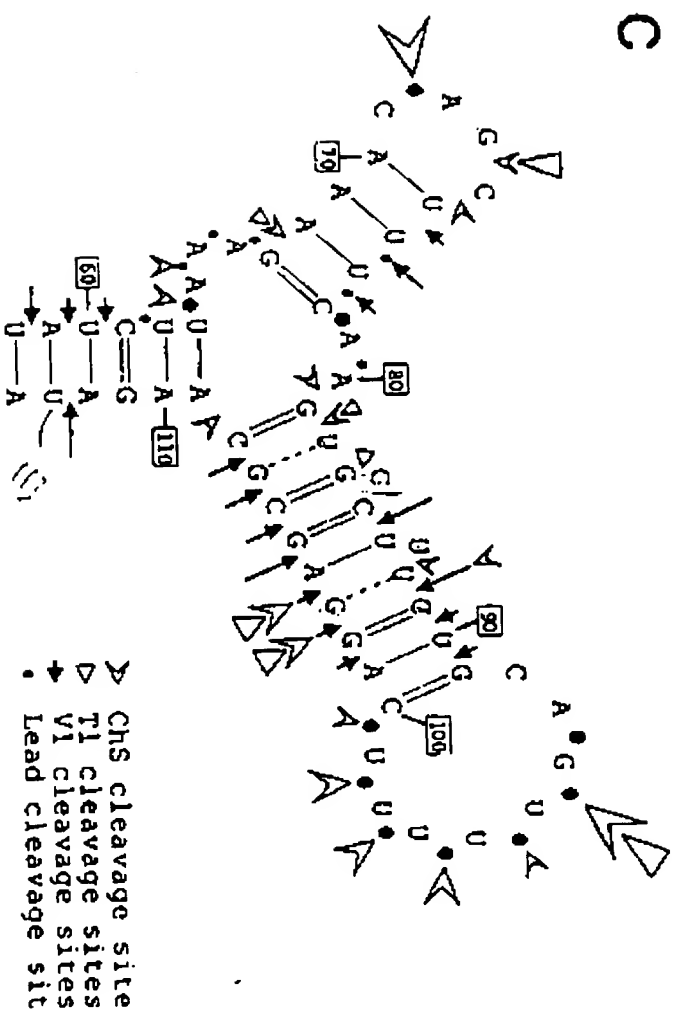


Figure 42

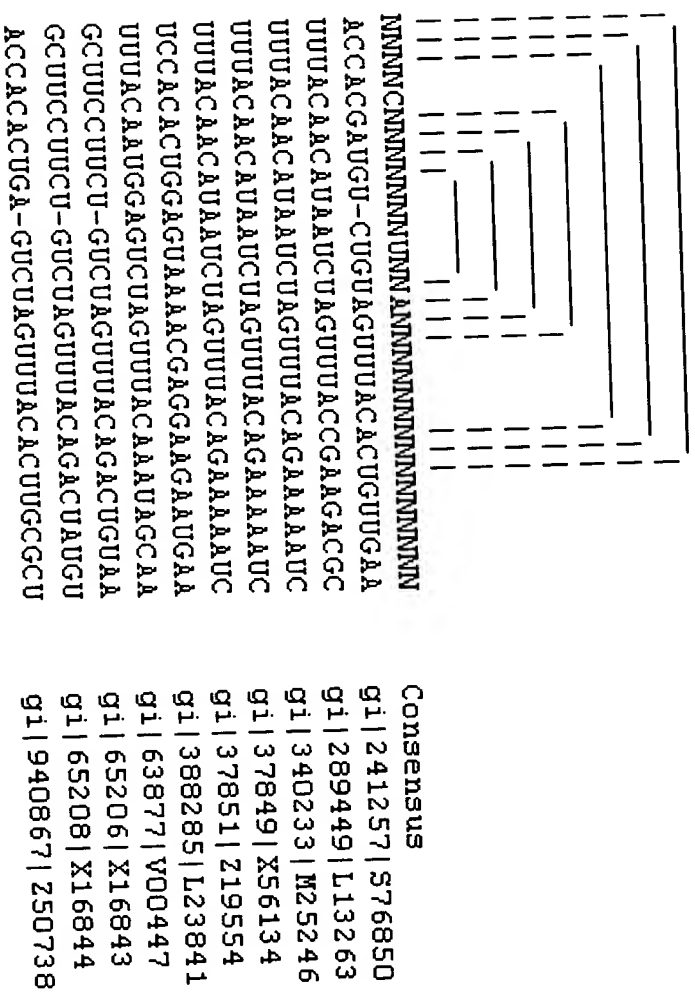


# Figure 43

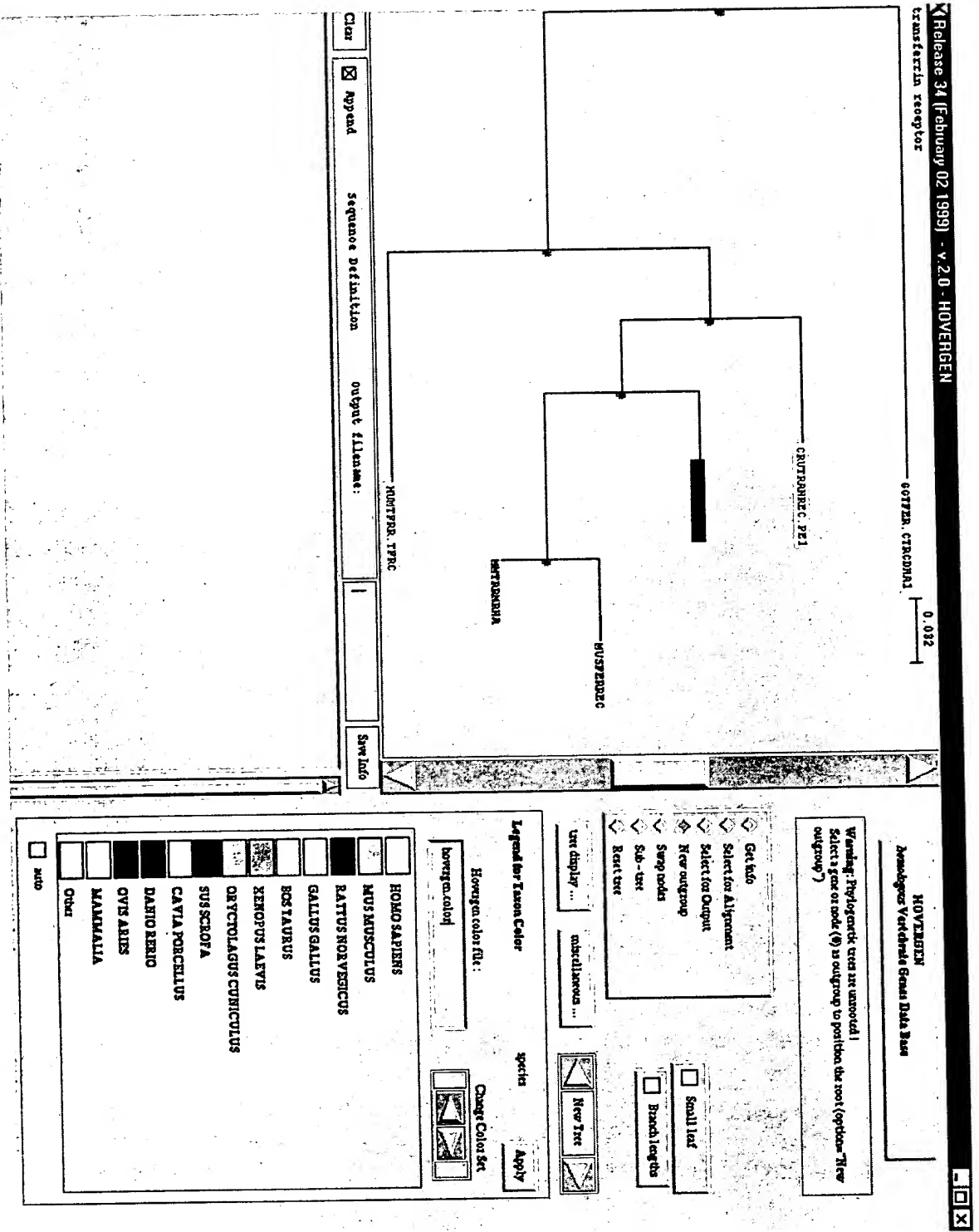
CLUSTAL W (1.74) multiple sequence alignment

```
qi|241257|S76850      ACCACGATGT-CTGTAGTTTACACTGTTGAA
qi|289449|L13263      TTTACAACATAATCTAGTTTACCGAAGACGC
qi|340233|M25246      TTTACAACATAATCTAGTTTACAGAAAAATC
qi|37849|X56134       TTTACAACATAATCTAGTTTACAGAAAAATC
qi|37851|Z19554       TTTACAACATAATCTAGTTTACAGAAAAATC
qi|388285|L23841      TCCACACTGGAGTAAACGAGGAAGAAATGAA
qi|63877|V00447       TTTACAATGGAGTCTAGTTTACAAATAGCAA
qi|65206|X16843       GCTTCCTTCT-GTCTAGTTTACAGACTGTAA
qi|65208|X16844       GCTTCCTTCT-GTCTAGTTTACAGACTATGT
qi|940867|Z50738      ACCACACTGA-GTCTAGTTTACACTTGGCCT
```

# Figure 44



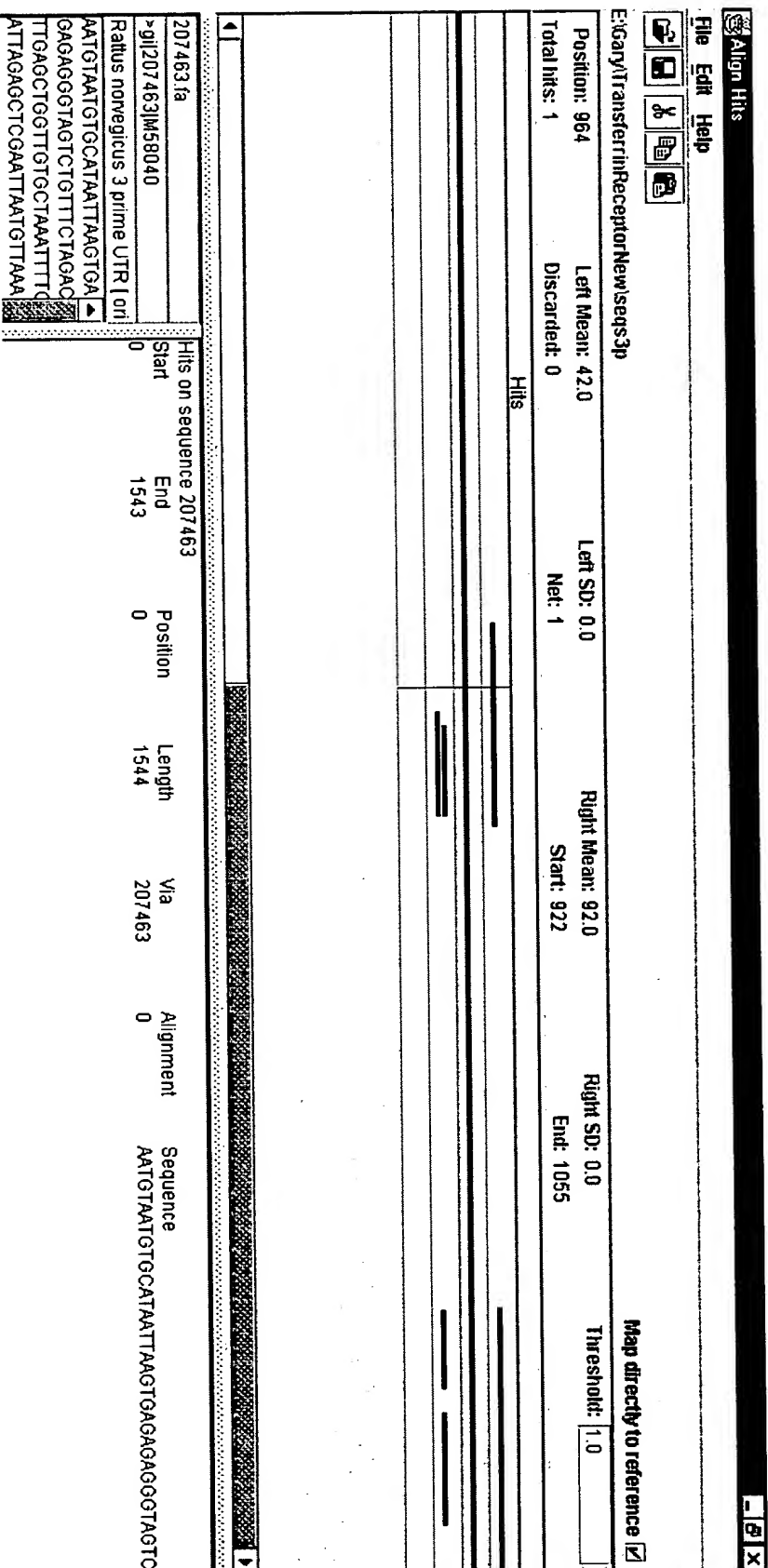
# Figure 45



09310667.051299



# Figure 46



09310667.051299

## Figure 47

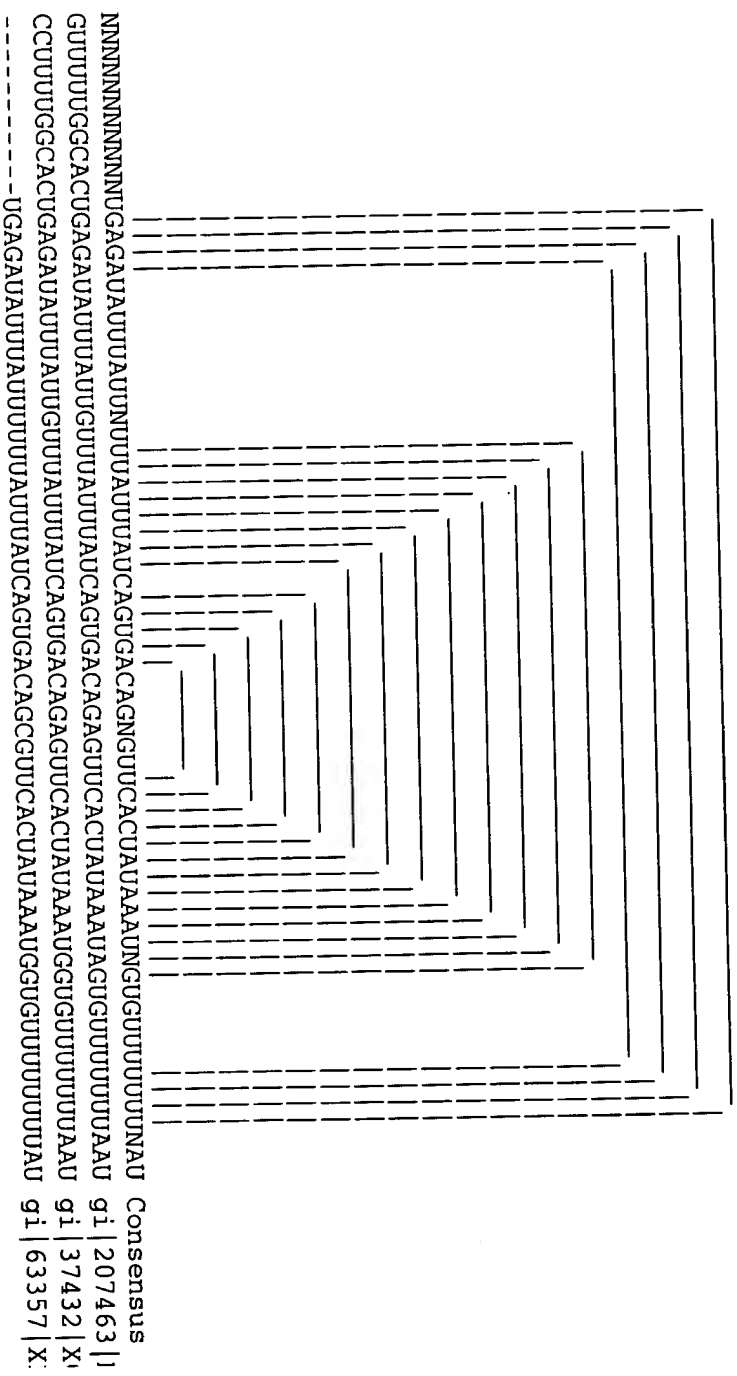
CLUSTAL W (1.74) multiple sequence alignment

```
gi|207463|M58040
GTTTTGGCAGTGAATATTTATGTTTATTTATCAGTGACAGAGTTCACTATAAATAGTGTGTTTTTAAT
gi|37432|X01060
CCTTTGGCAGTGAATATTTATGTTTATTTATCAGTGACAGAGTTCACTATAAATGGTGTGTTTTTAAT
gi|63357|X13753      -----
TGAGATATTTATTTTATTTATCAGTGACAGCGTTCACCTATAAATGGTGTGTTTTTAAT
```

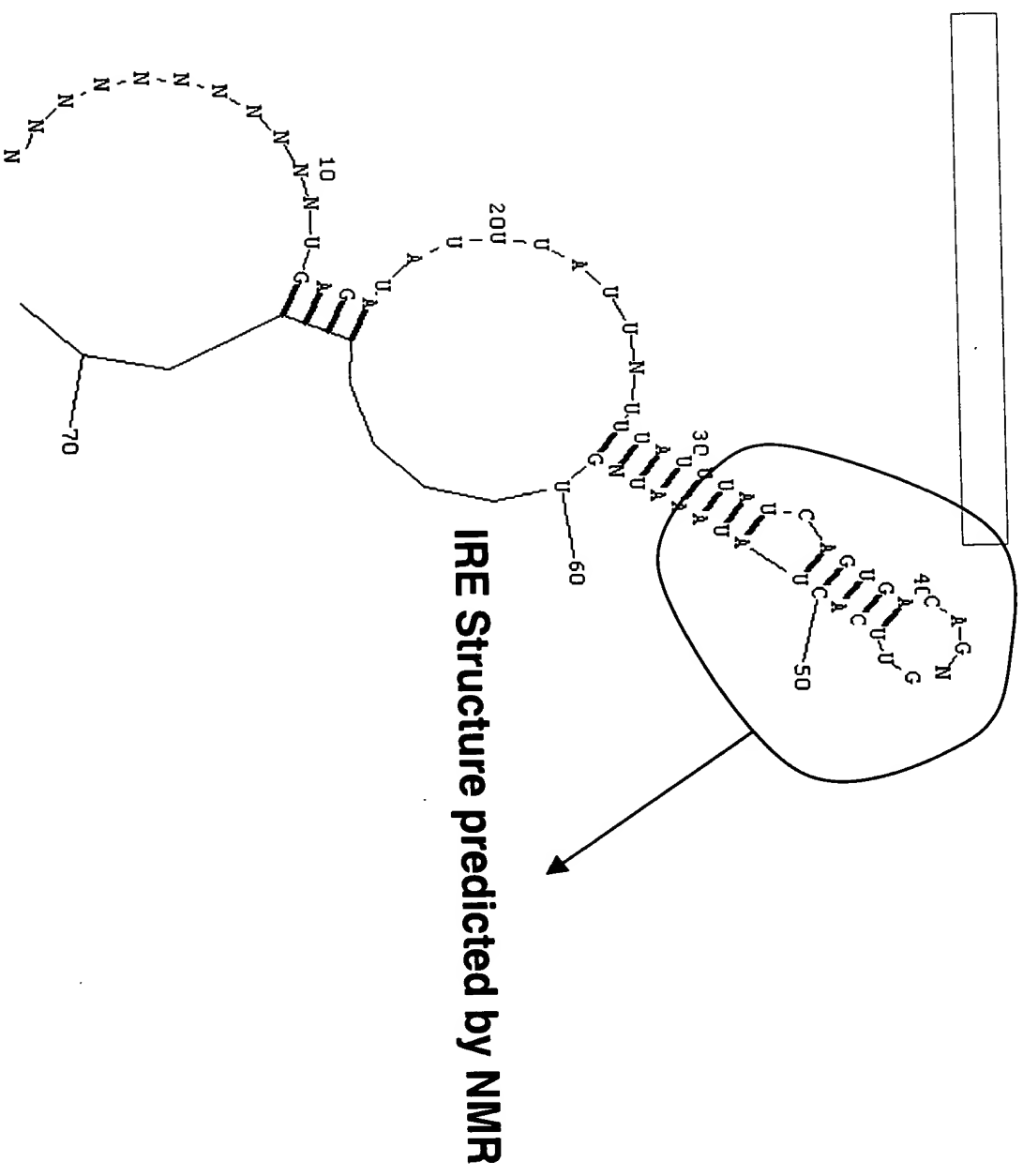
09310667.051299

Figure 48

Score: 102.0

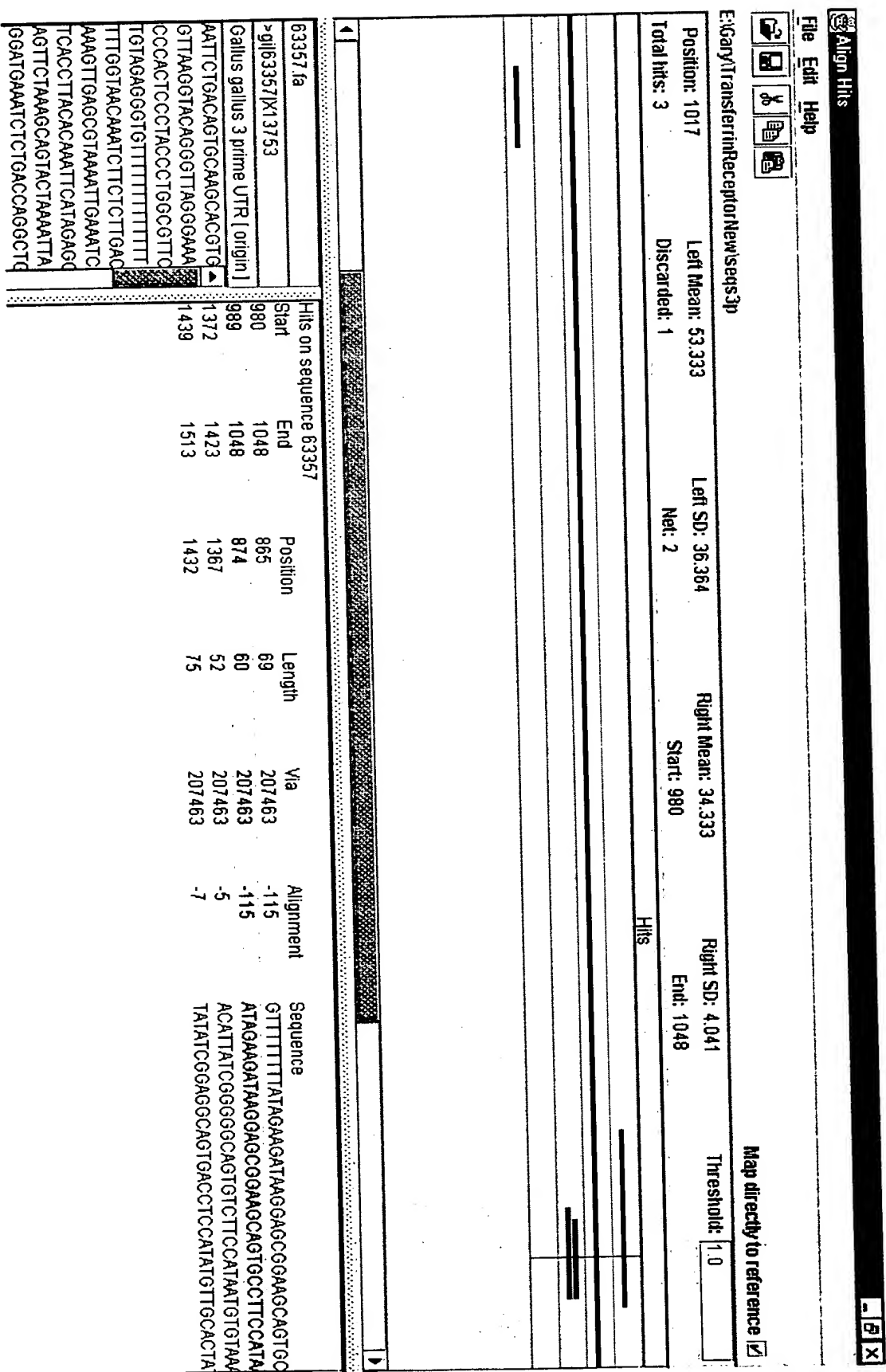


**Figure 49**



09310667-051299

# Figure 50



09310657.051299

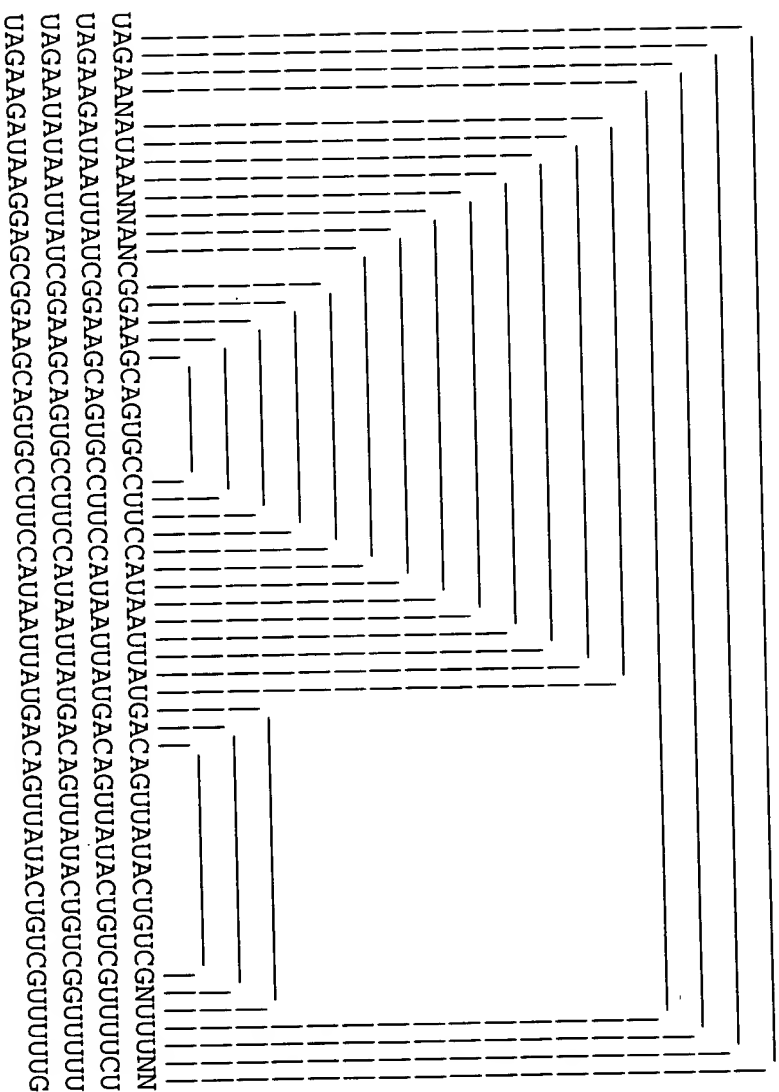
## Figure 51

CLUSTAL W (1.74) multiple sequence alignment

```
gi|207463|M58040
TAGAAGATAATTATCGGAGCAGTGCCCTTCATAATTATGACAGTTATACTGTCGTTTCT
gi|37432|X01060
TAGAATATAATTATCGGAGCAGTGCCCTTCATAATTATGACAGTTATACTGTCGTTTCT
gi|63357|X13753
TAGAAGATAAGAGCGGAGCAGTGCCCTTCATAATTATGACAGTTATACTGTCGTTTCT
```

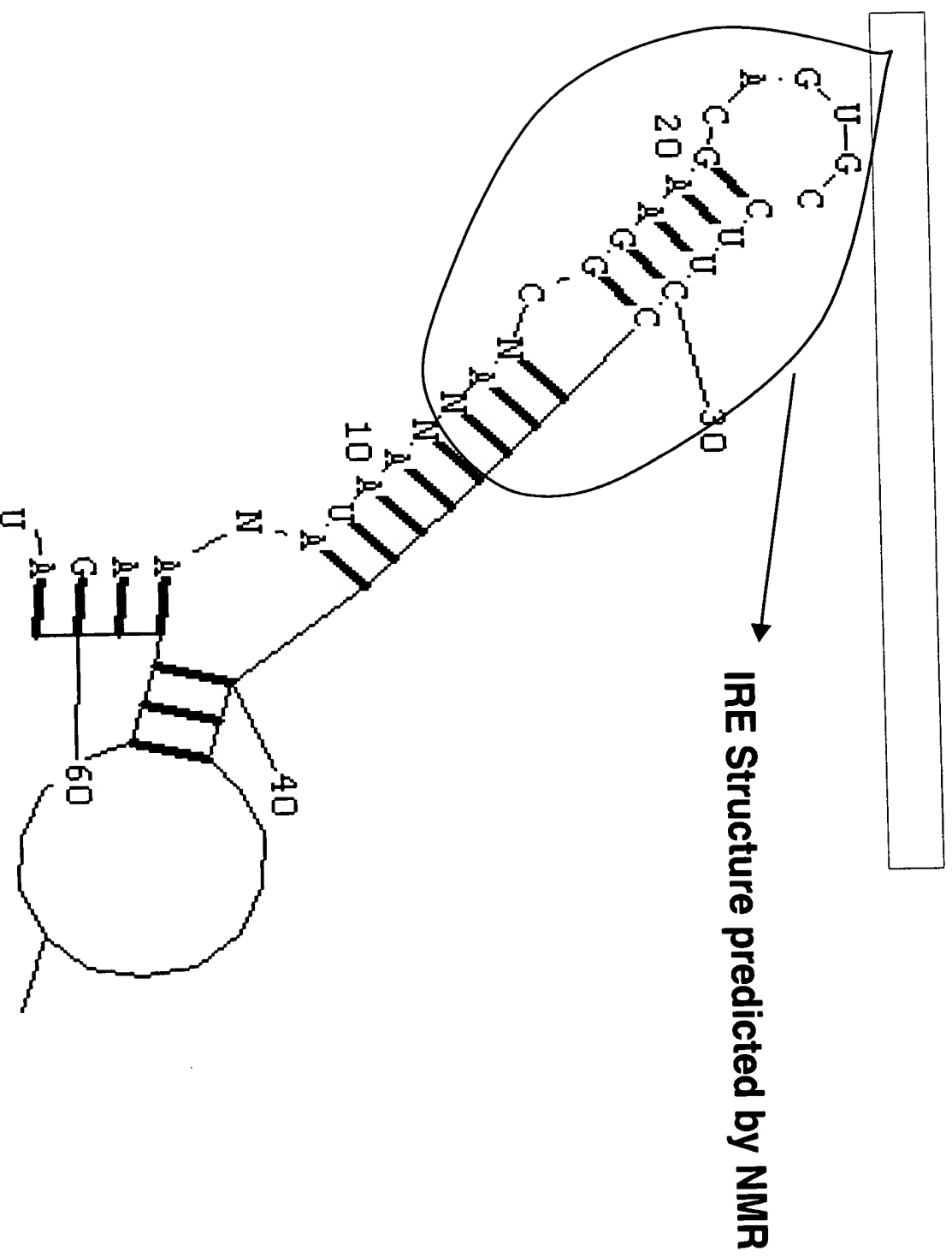
Figure 52

Score: 115.0



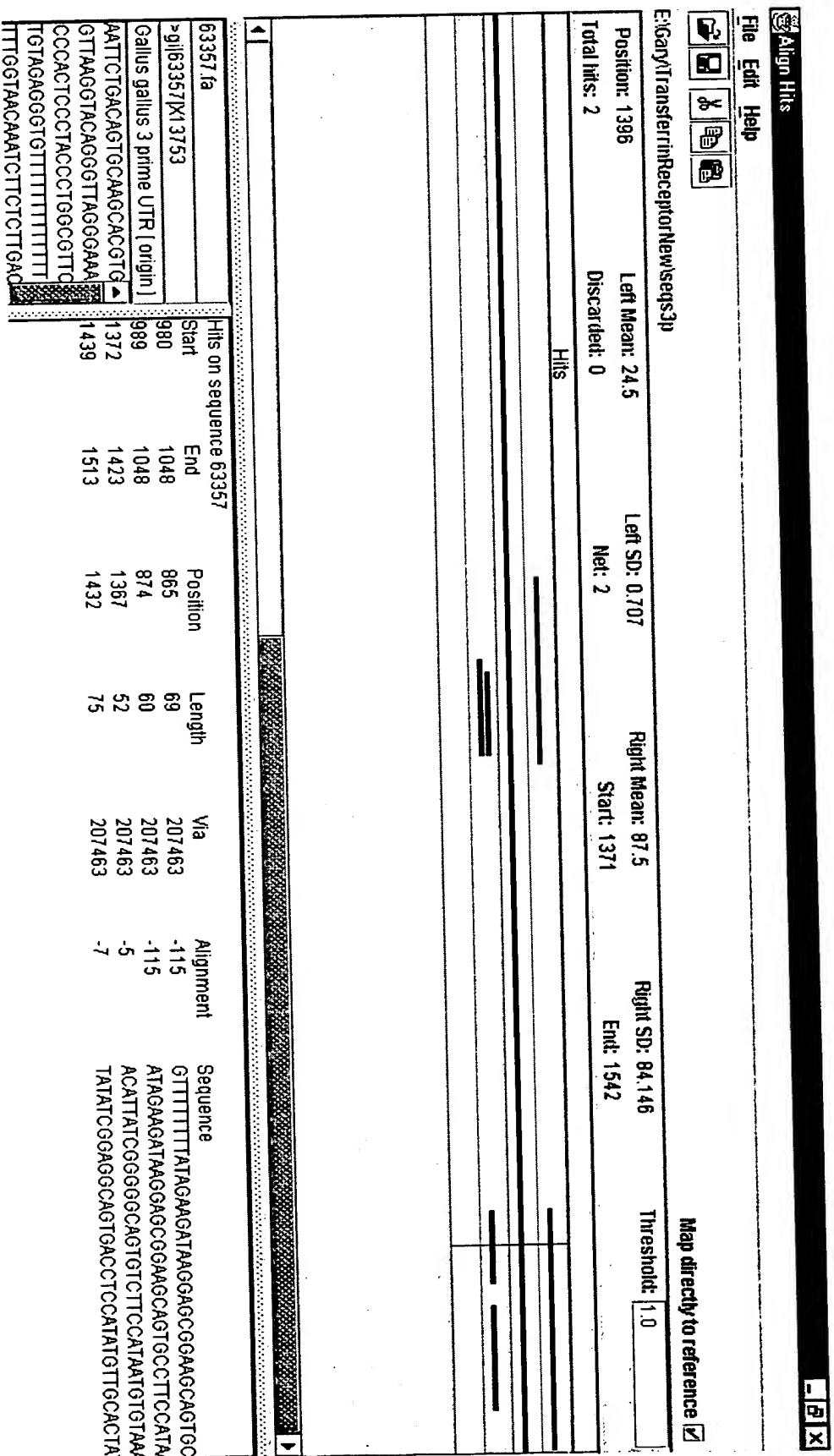
Consensus  
gi | 207463 | M58040  
gi | 37432 | X01060  
gi | 63357 | X13753

Figure 53





# Figure 54



09310657.051299

# Figure 55

CLUSTAL W (1.74) multiple sequence alignment

```
gi|207463|M58040      ACATTATCGGGAGCAGTGTCTTCCATAATGTATAAAGACAAGGTAGTTTTT
gi|37432|X01060      ACATTATCGGGAGCAGTGTCTTCCATAATGTATAAAGACAAGGTAGTTTTT
gi|63357|X13753      ACATTATCGGGGCAGTGTCTTCCATAATGTATAAAGACAAGGTAGTTTTT
*****
```

Figure 56

Score: 108.0

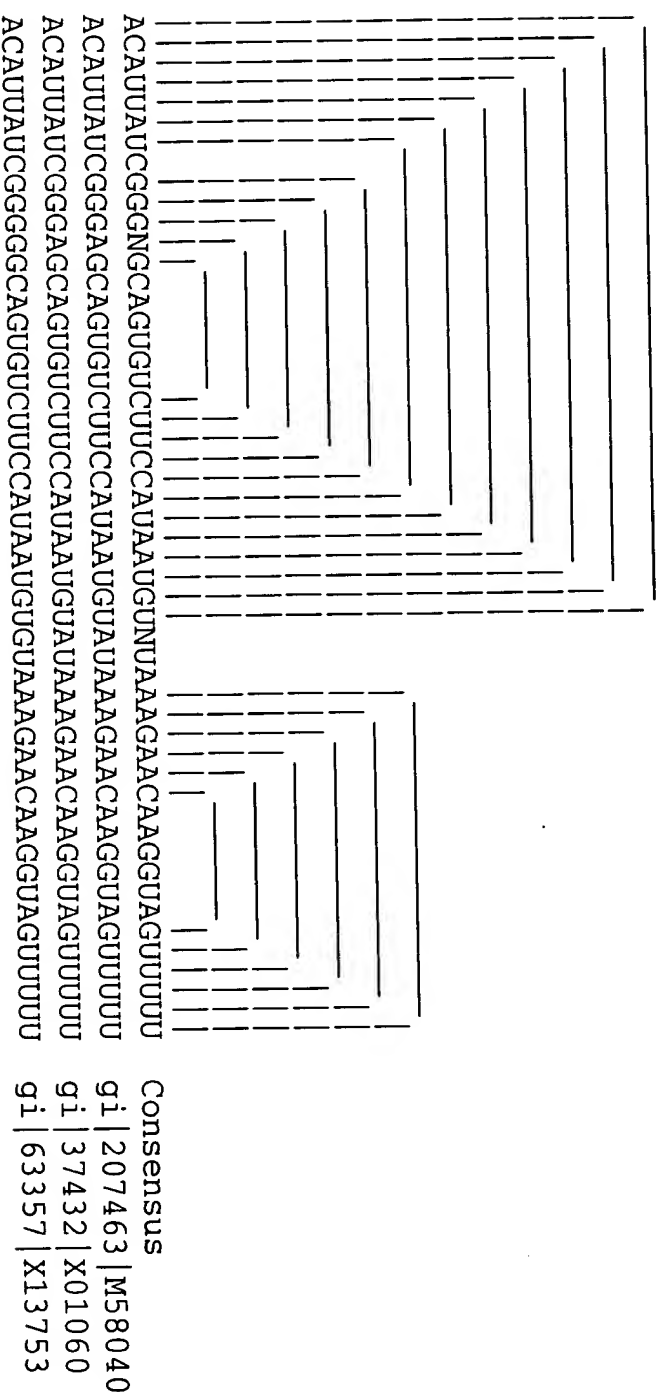
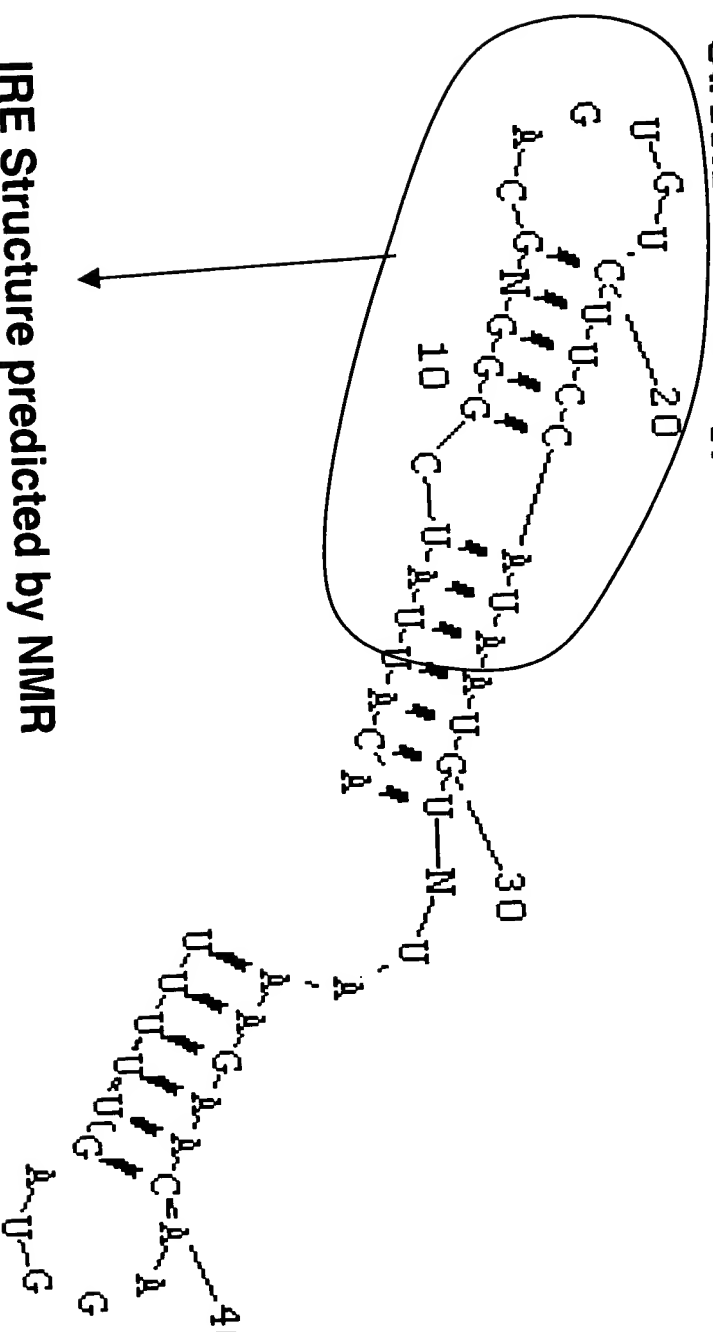


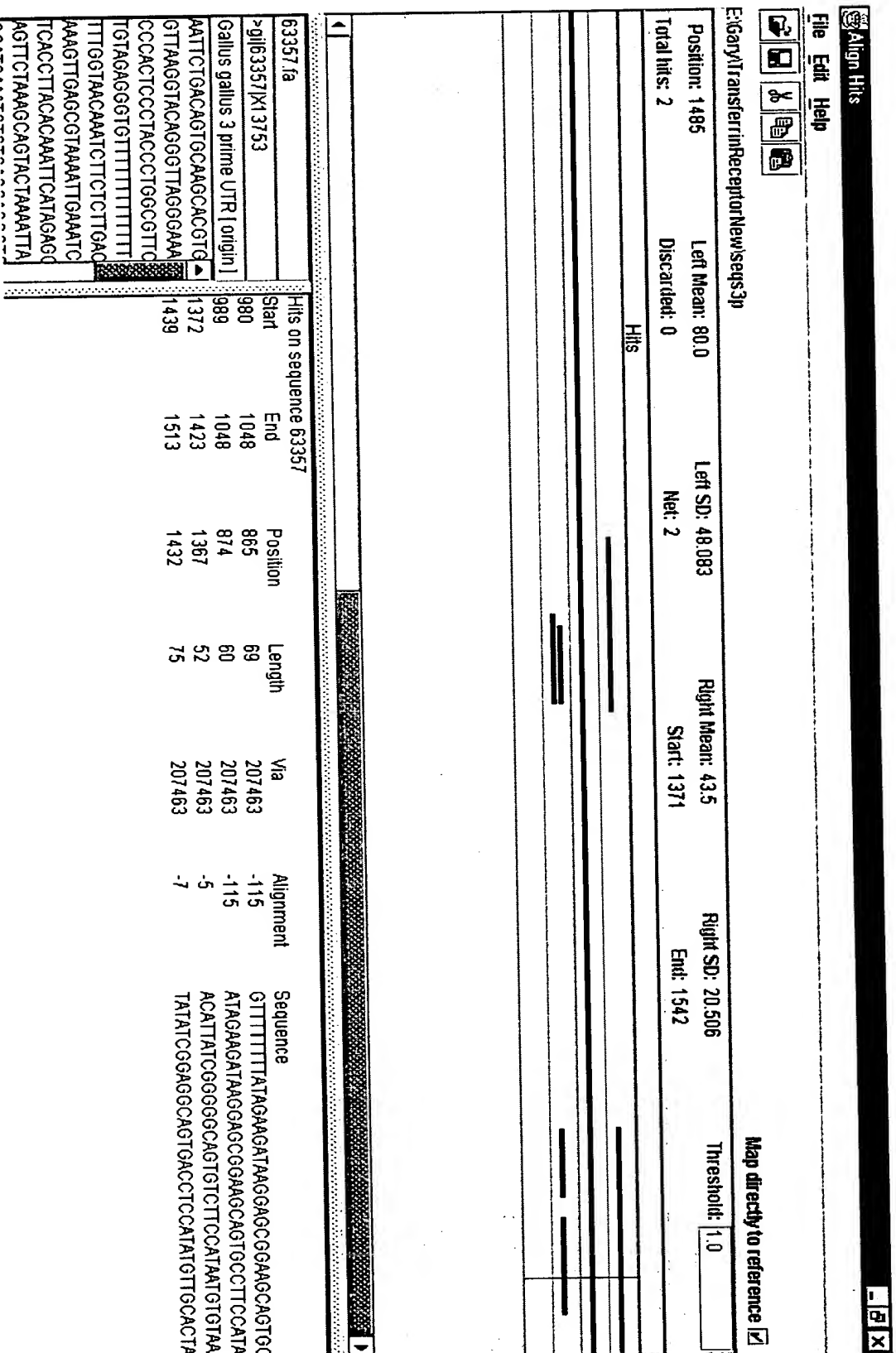
Figure 57

Structure: 1 Energy = 108.0 nothing to say !



09310667.051299

Figure 58



09310667.051299

## Figure 59

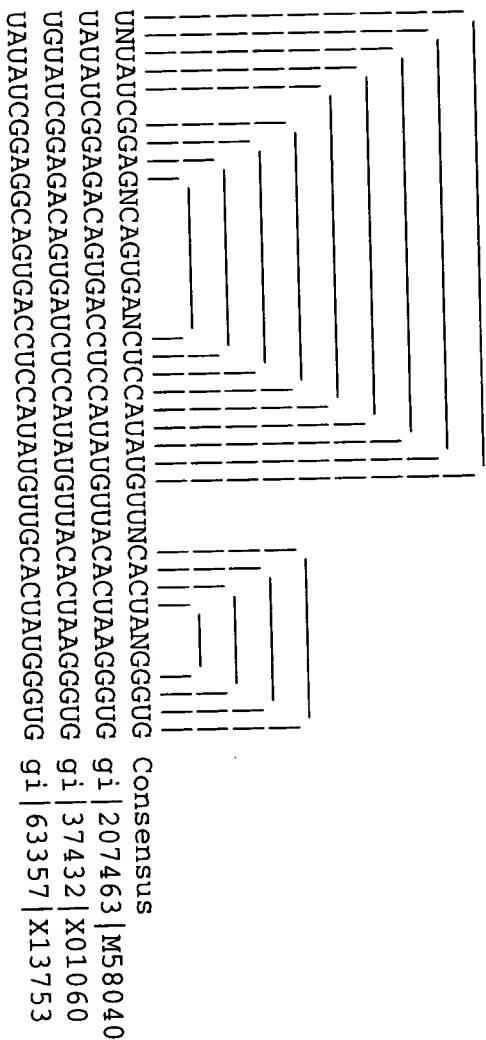
CLUSTAL W (1.74) multiple sequence alignment

```
gi|207463|M58040      TATATCGAGACAGTGACCTCCATATGTGTACACTAAGGCTG
gi|37432|X01060      TGTATCGAGACAGTGATCTCCATATGTGTACACTAAGGCTG
gi|63357|X13753      TATATCGAGGCGAGTGACCTCCATATGTGTGCACTATGGGTG
* * * * *
* * * * *
```

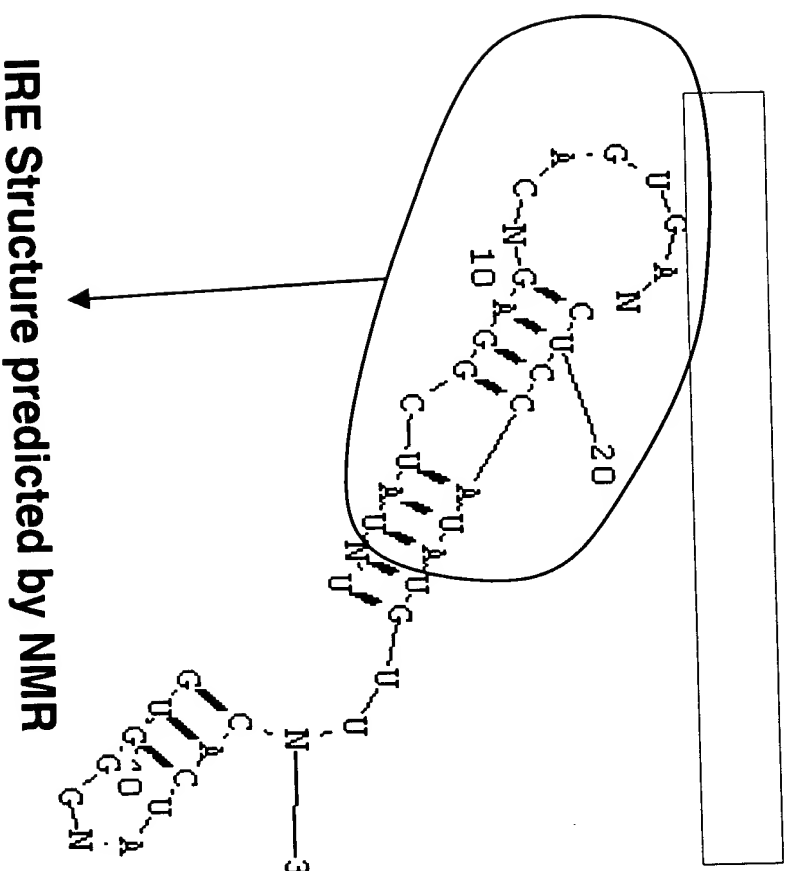
09310657.051299

Figure 60

Score: 78.0

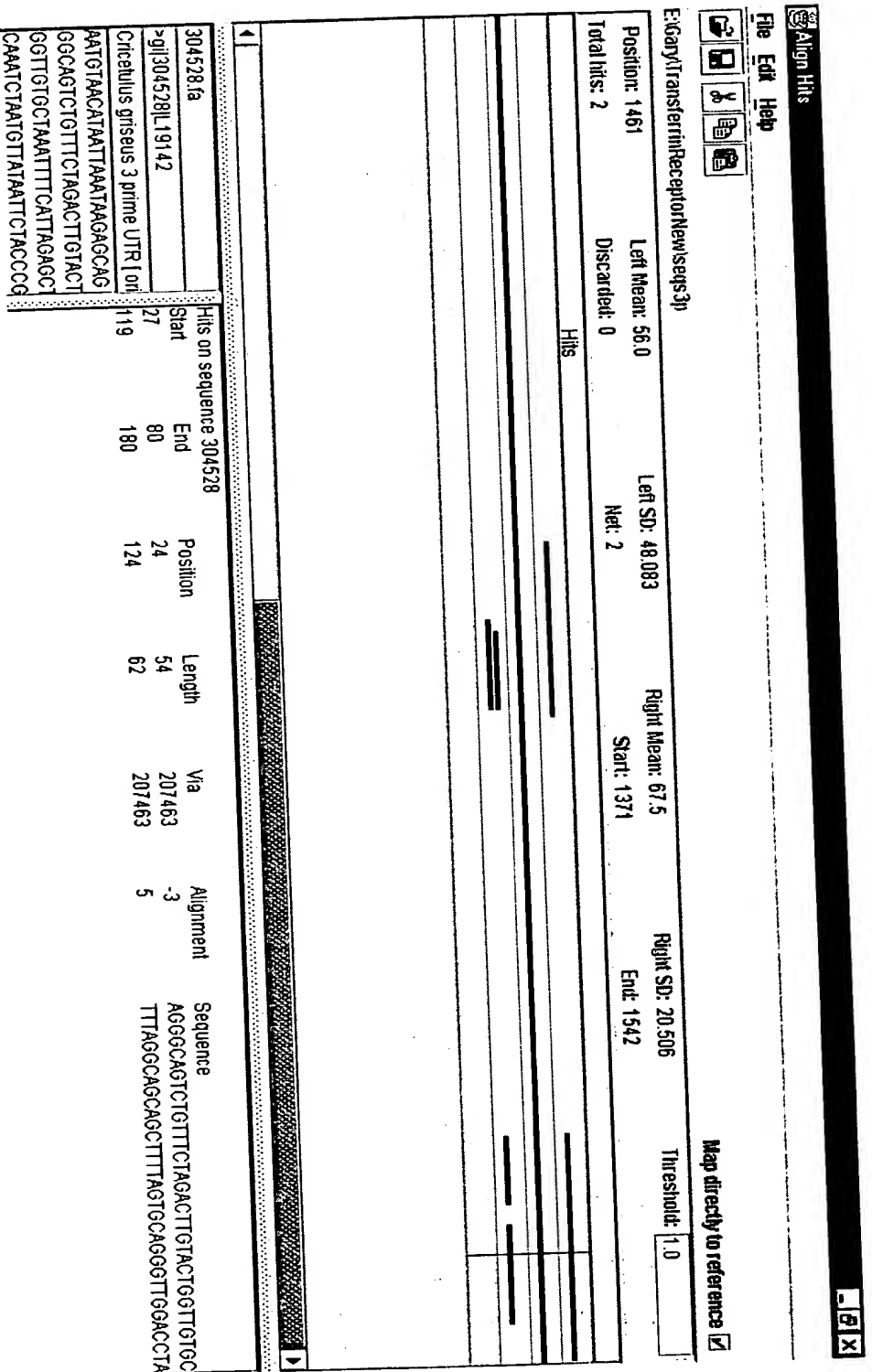


**Figure 61**





# Figure 62



09310567.051299

## Figure 63

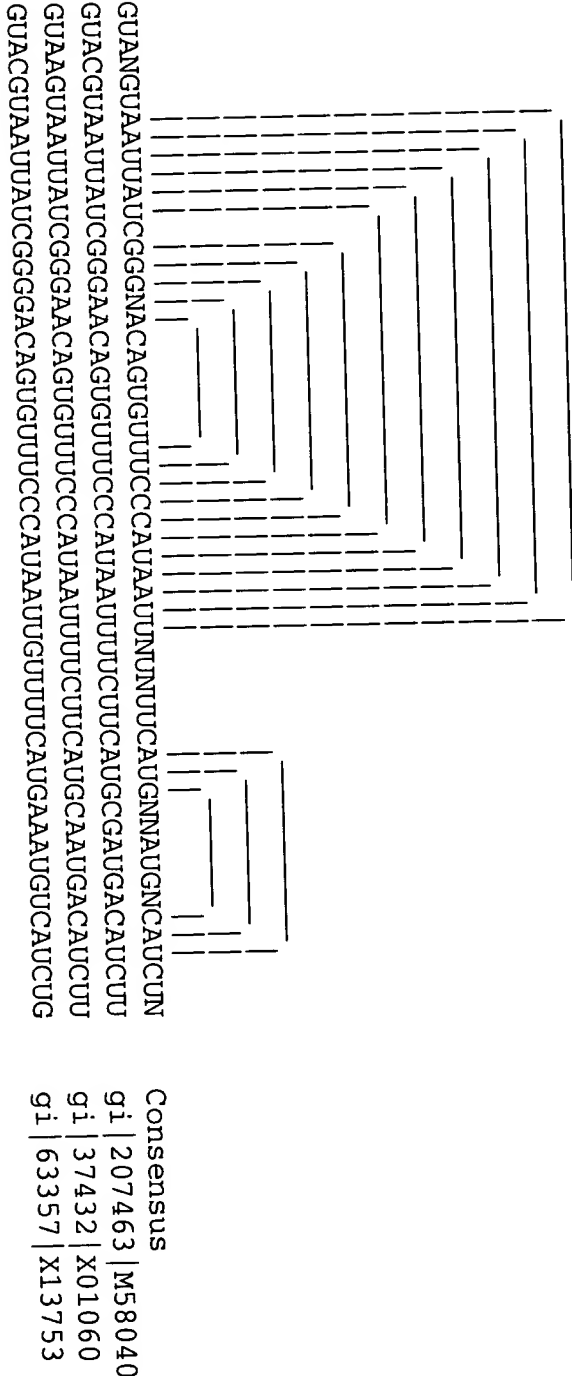
CLUSTAL W (1.74) multiple sequence alignment

```
gi|207463|M58040      GTACGTAATTATCGGGACAGTGTTCCCATAATTTCTTCATGCGATGACATCTT
gi|37432|X01060      GTAAGTAATTATCGGGACAGTGTTCCCATAATTTCTTCATGCAATGACATCTT
gi|63357|X13753      GTACGTAATTATCGGGACAGTGTTCCCATAATTGTTTTCATGAAATGTCATCTG
```

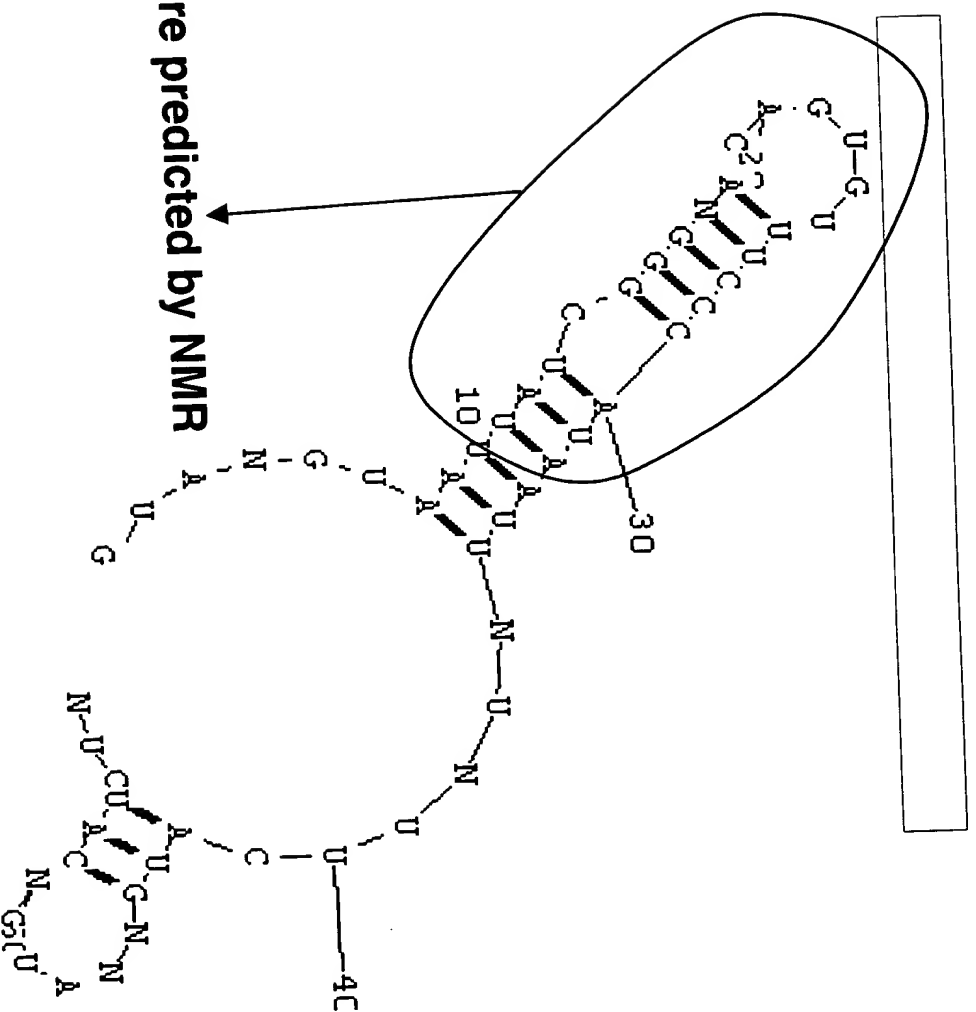
09310667.051299

Figure 64

Score: 84.0

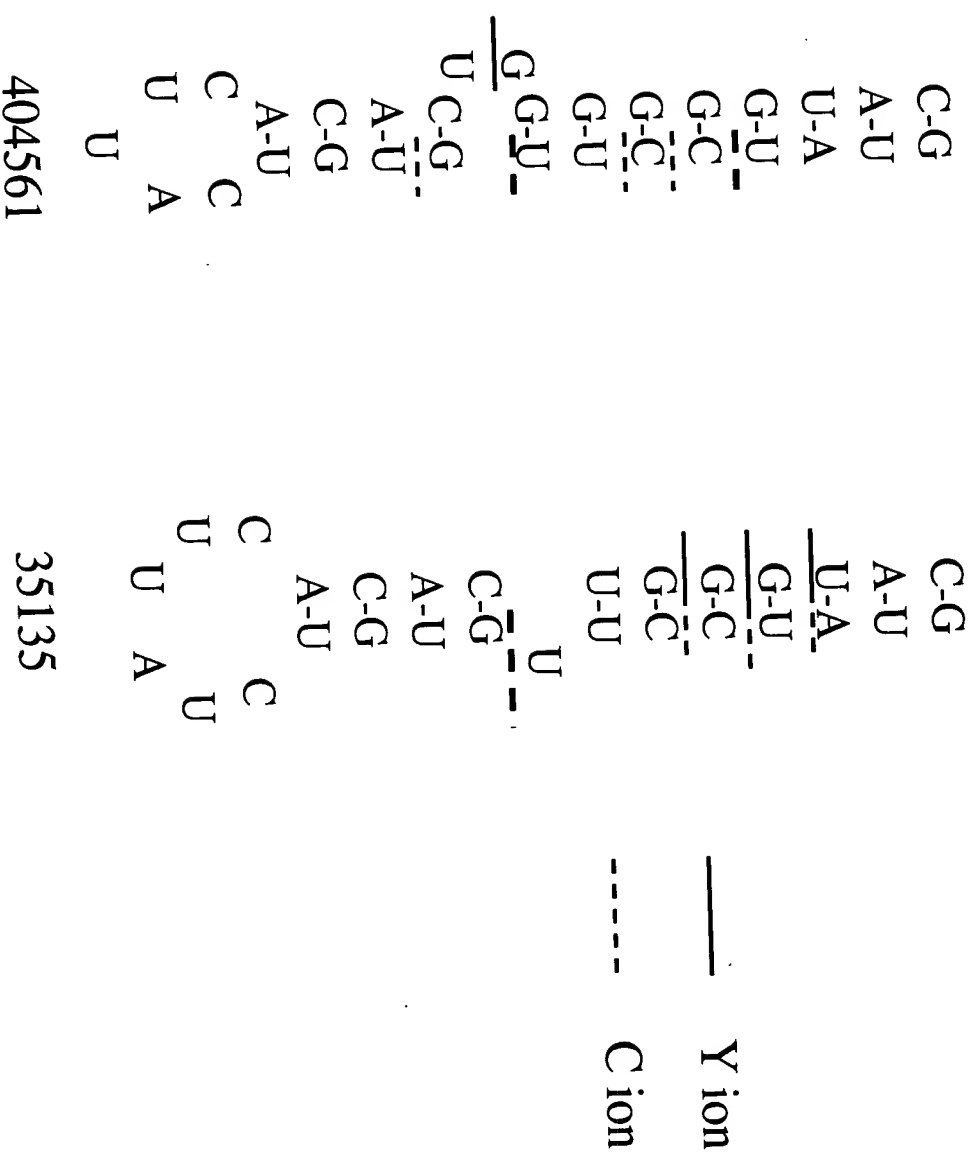


**Figure 65**



09310667.051299

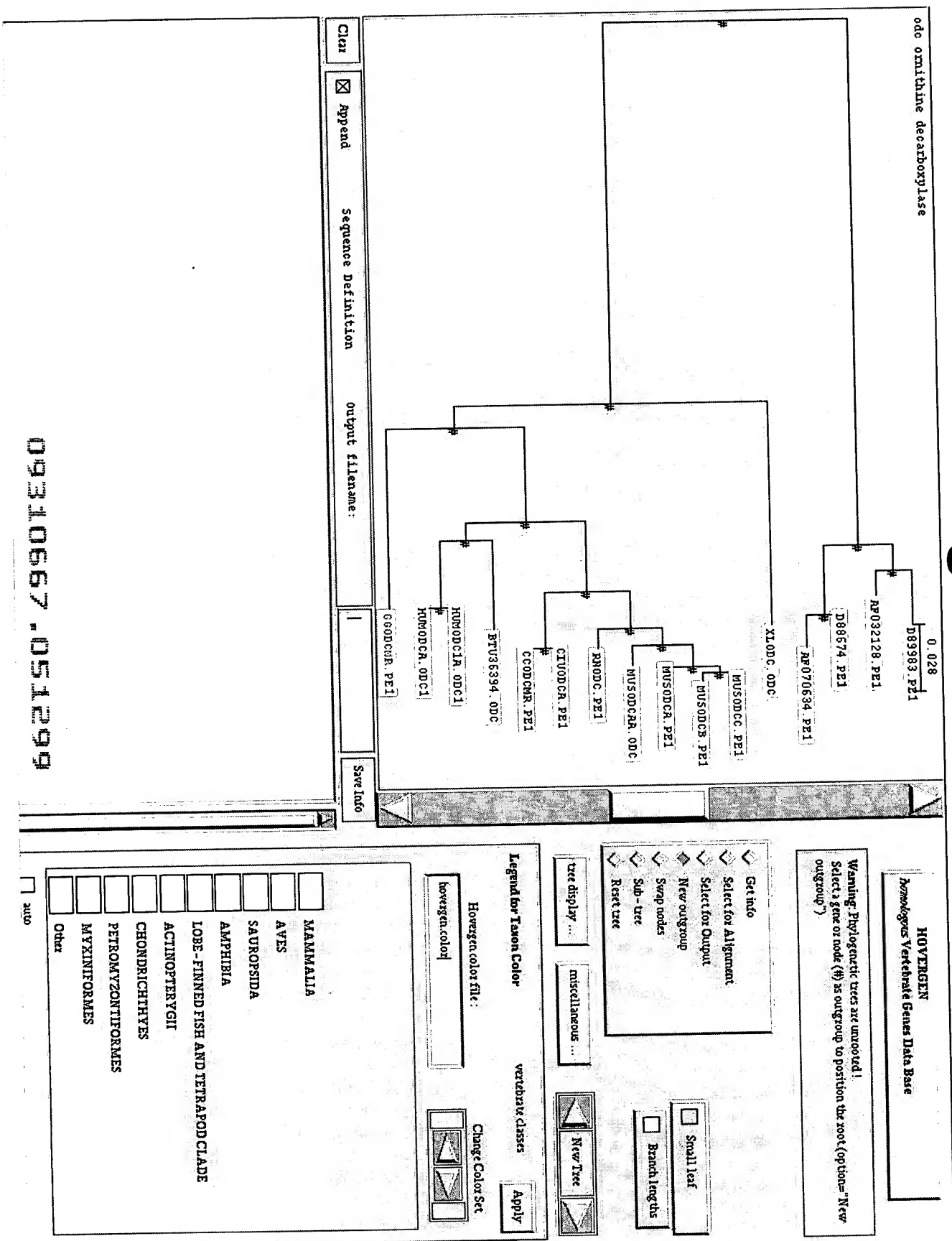
Figure 66



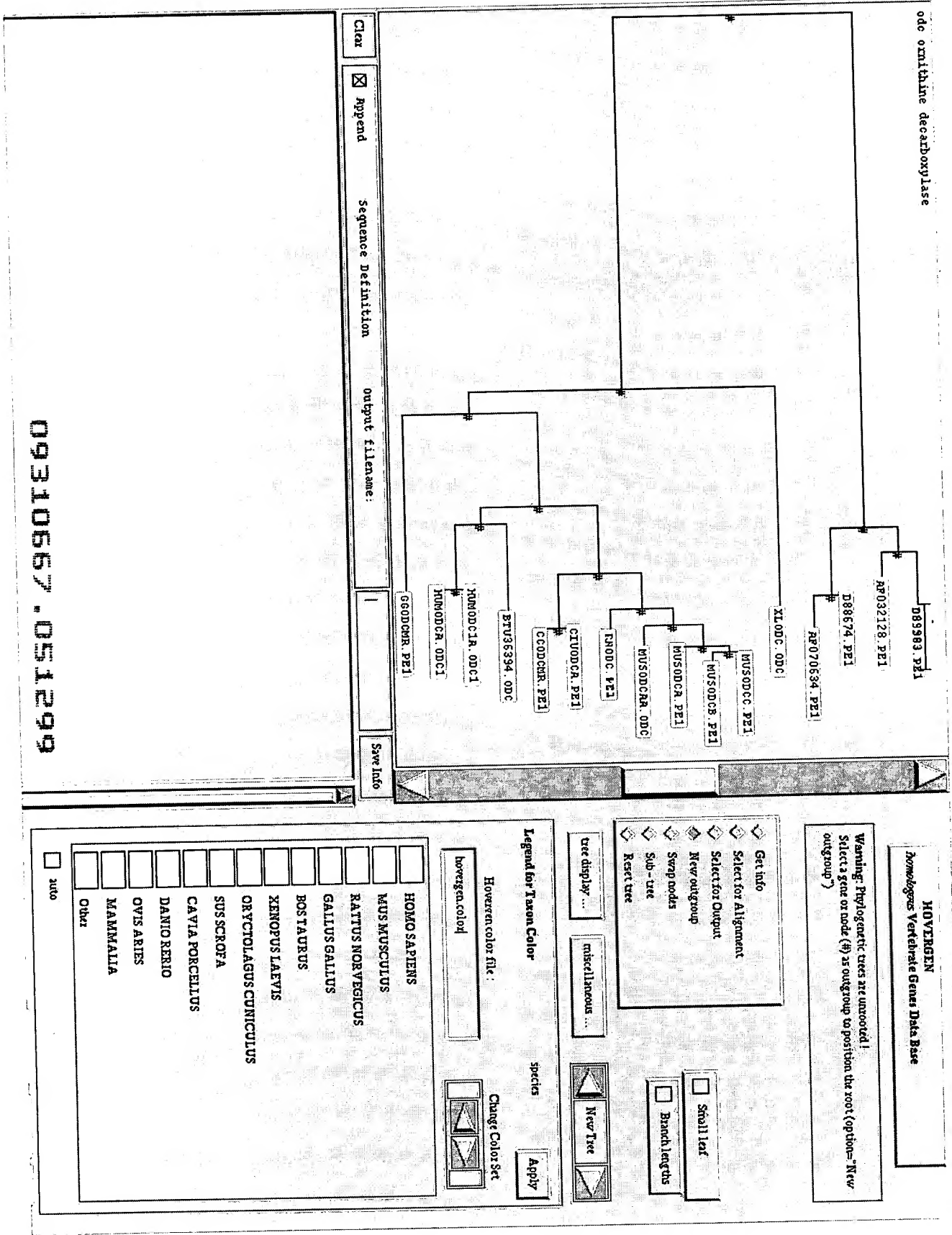
# Figure 67

A	
1	CLUSTAL W (1.74) multiple sequence alignment
2	
3	
4	gi 163448 M92441 -ACTGGGAGATGGG--TCACACTTATCTGTGTTCCCTATGGAACCTATTGAATAT----
5	gi 163448 M92441b ---TGGGAGATGGG--TCACACTTATCTGTGTTCCCTATGGAACCTATTGAATATT--
6	gi 200123 M87223 -CTAGAAGATGGGG--TCACACTTA-CTGTGTTCCCTATGGAACCT--TTGAATATTGT-
7	gi 200123 M87223b ---TAGAAGATGGGG--TCACACTTA-CTGTGTTCCCTATGGAACCT--TTGAATATTGT-
8	gi 205807 J04791 --CTAGGAGATGGGG--TCACACTTA-CTGTGTTCCCTATGGAACCT--TTGAATATTGTA
9	gi 205807 J04791b ---TAGGAGATGGGG--TCACACTTA-CTGTGTTCCCTATGGAACCT--TTGAATATTGTA
10	gi 35135 X55362 ---CTAGGATATGGG--TCACACTTATCTGTGTTCCCTATGGAACCT--TTGAATATTGTA
11	gi 404561 S64539 ----ACGAGATGGGGGTCACACTTA-CTGTGTTCCCTATGGAACCT--TTGAATATTGTA
12	gi 404561 S64539b ---TAGGAGATGGGGGTCACACTTA-CTGTGTTCCCTATGGAACCTATTGGAATATTG--
13	gi 63712 X64710 --CTAGGAGATGGG--TCACATTTATCTGTGTTCCCTATGGAACCTATTGGAATATTG--
14	gi 63712 X64710b GACTAGGAGATGGG--TCACATTTATCTGTGTTCCCTATGGAACCTATTGGAATATTG--
15	gi 64953 X56316 -ACTCGGAGATGGG--TCACA--TATCTGTGTTCCCTATGGAACCTTTTTTTTC--
16	* **** * * * * *
17	NNNNNNANATGGNNNTCACANNNTANCTGTGTTCCCTATGGAACCTNNNTNNNTNNNN
18	

# Figure 68



# Figure 69



09310667.051299



# Figure 70

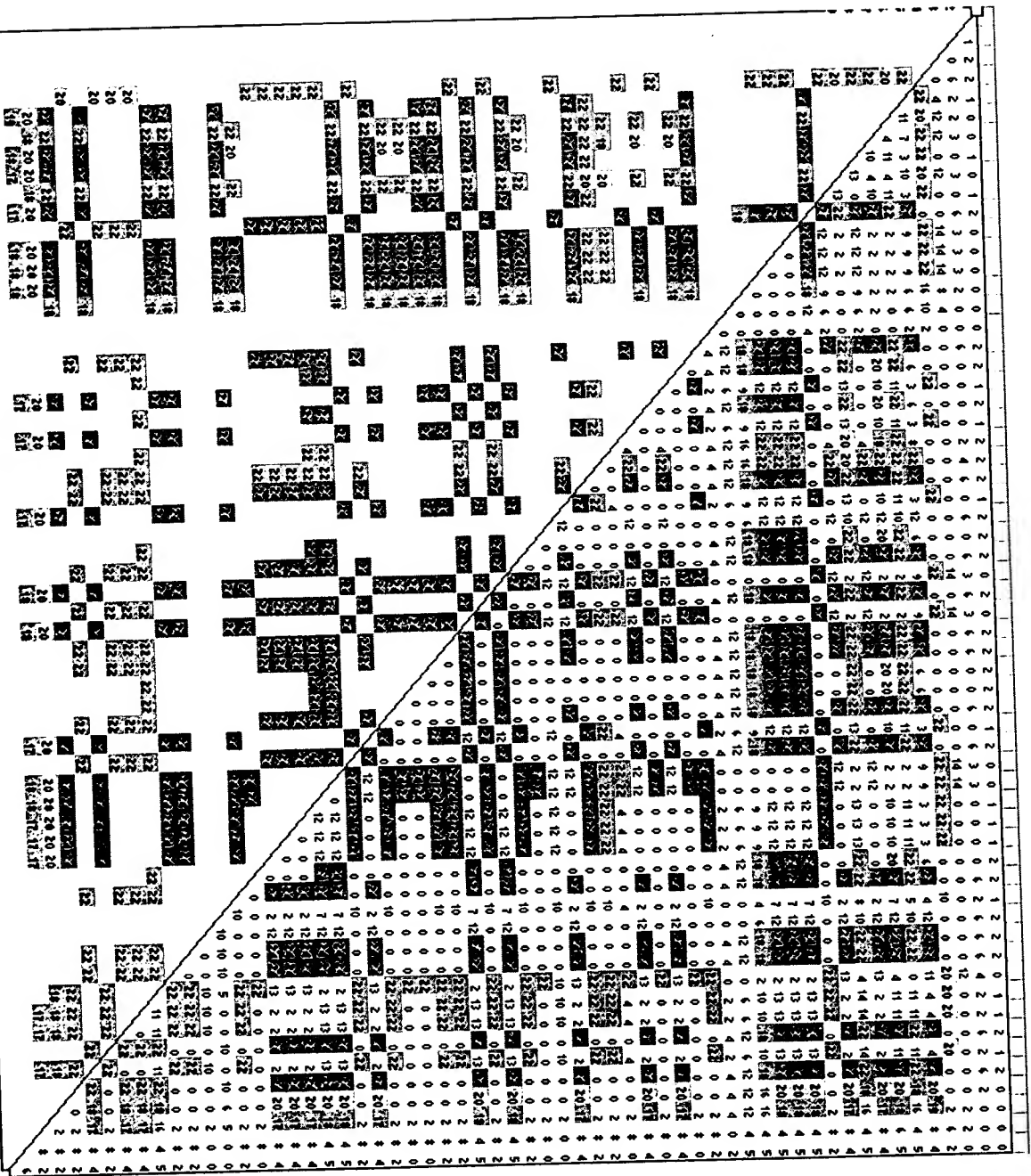
J:\cowxTargets\35135\seqs3p

Position:	Left Mean:	Left SD:	Right Mean:
Total hits:	Discarded:	Net:	Start:
Number	Description	Hits	
<input type="checkbox"/> 35135.fa	Homo sapiens 3 prime UTR ...	—	—
<input checked="" type="checkbox"/> 64953.fa	Xenopus laevis 3 prime UTR...	—	—
<input type="checkbox"/> 162173.fa	Trypanosoma brucei 3 prime...	—	—
<input type="checkbox"/> 163448.fa	Bos taurus 3 prime UTR [ori...	—	—
<input type="checkbox"/> 205807.fa	Rattus norvegicus 3 prime U...	—	—
<input type="checkbox"/> 404561.fa	Mus musculus domesticus ...	—	—
<input type="checkbox"/> 63712.fa	Gallus gallus 3 prime UTR [ ...	—	—
<input type="checkbox"/> 200123.fa	Mus pahari 3 prime UTR [ori...	—	—
<input type="checkbox"/> 2337849.fa	Ustilago maydis 3 prime UT...	—	—

Region 1

Region 2

Figure 71



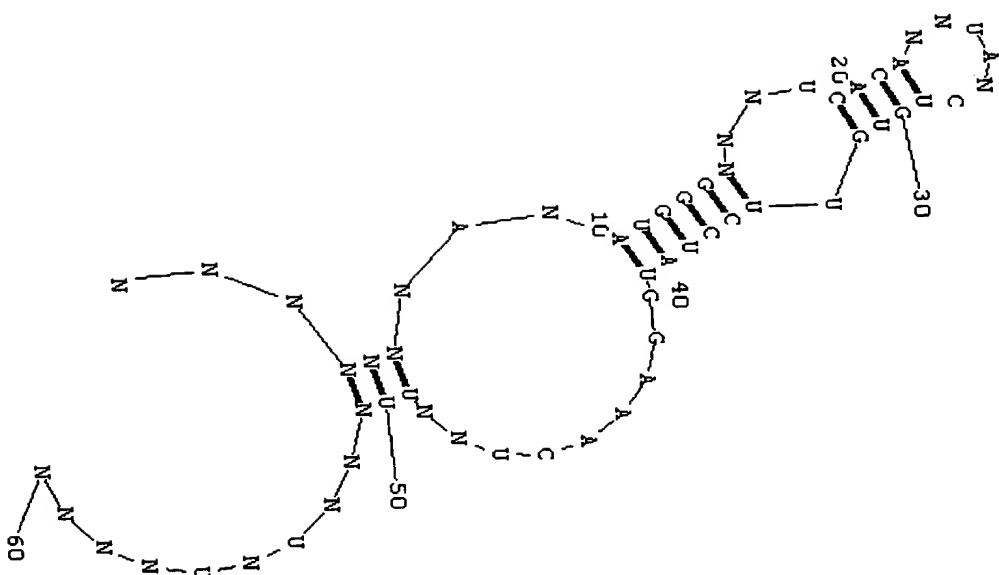
09310667-051299

\_\_\_\_\_

Consensus  
gi | 163448 | M92441  
gi | 163448 | M92441b  
gi | 200123 | M87223  
gi | 200123 | M87223b  
gi | 205807 | J04791  
gi | 205807 | J04791b  
gi | 205807 | J04791b  
gi | 351351 | X55362  
gi | 404561 | S64539  
gi | 404561 | S64539b  
gi | 63712 | X64710  
gi | 63712 | X64710b  
gi | 649551 | X56316

031067

Figure 73



09310667-051299

## Figure 74

CLUSTAL W (1.74) multiple sequence alignment

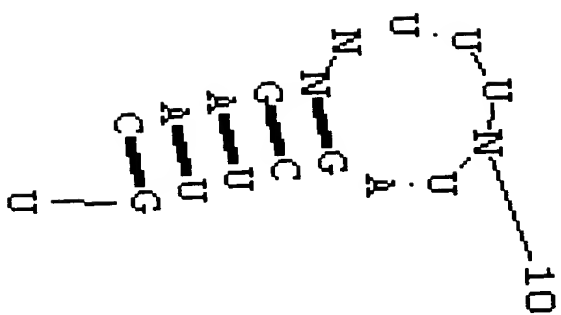
```
gi|404561|S64539      CAACCGTTGTAGCTTGT
gi|63712|X64710      CAAGTATTGTAGCTTGT
gi|64953|X56316      CAAGCATTGTAGCTTGT
gi|35135|X55362      CAAGCATTGTAGCTTGT
gi|200123|M87223      CAAGCATTGTAGCTTGT
gi|205807|J04791      CAAGCATTGTAGCTTGT
*****
```

# Figure 75

Score: 60.0

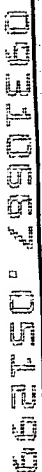
CAAGNMUUUUUAGCUUGU	Consensus
CAAGCGUUUGUAGCUUGU	gi 404561 S64539
CAAGUAUUUGUAGCUUGU	gi 63712 X64710
CAAGCAUUUGUAGCUUGU	gi 64953 X56316
CAAGCAUUUGUAGCUUGU	gi 35135 X55362
CAAGCAUUUAUAGCUUGU	gi 200123 M87223
CAAGCAUUUGUAGCUUGU	gi 205807 J04791

Figure 76



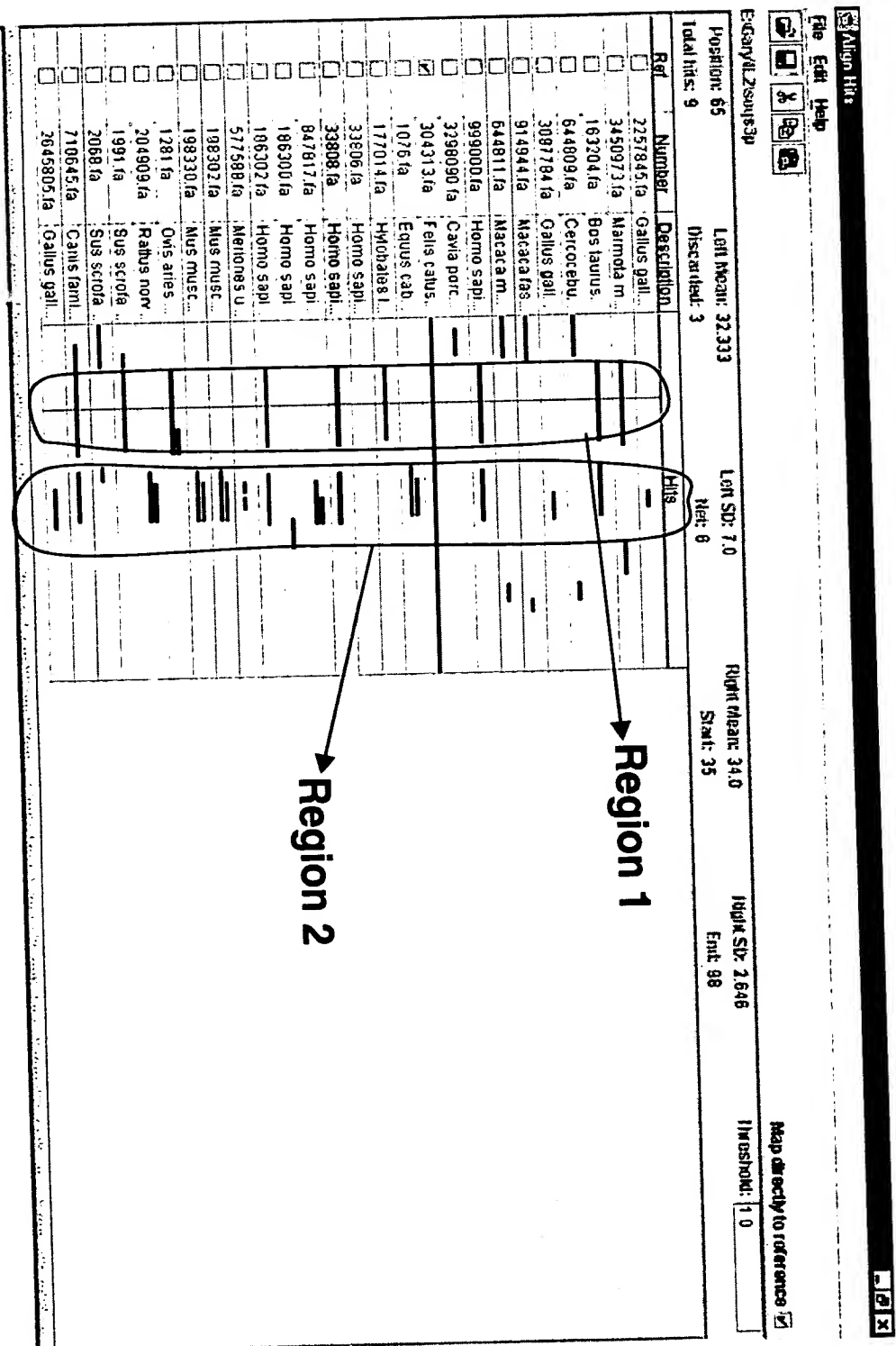
09310667.051299

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Interlockin-2





# Figure 78



09310667-051299

# Figure 79

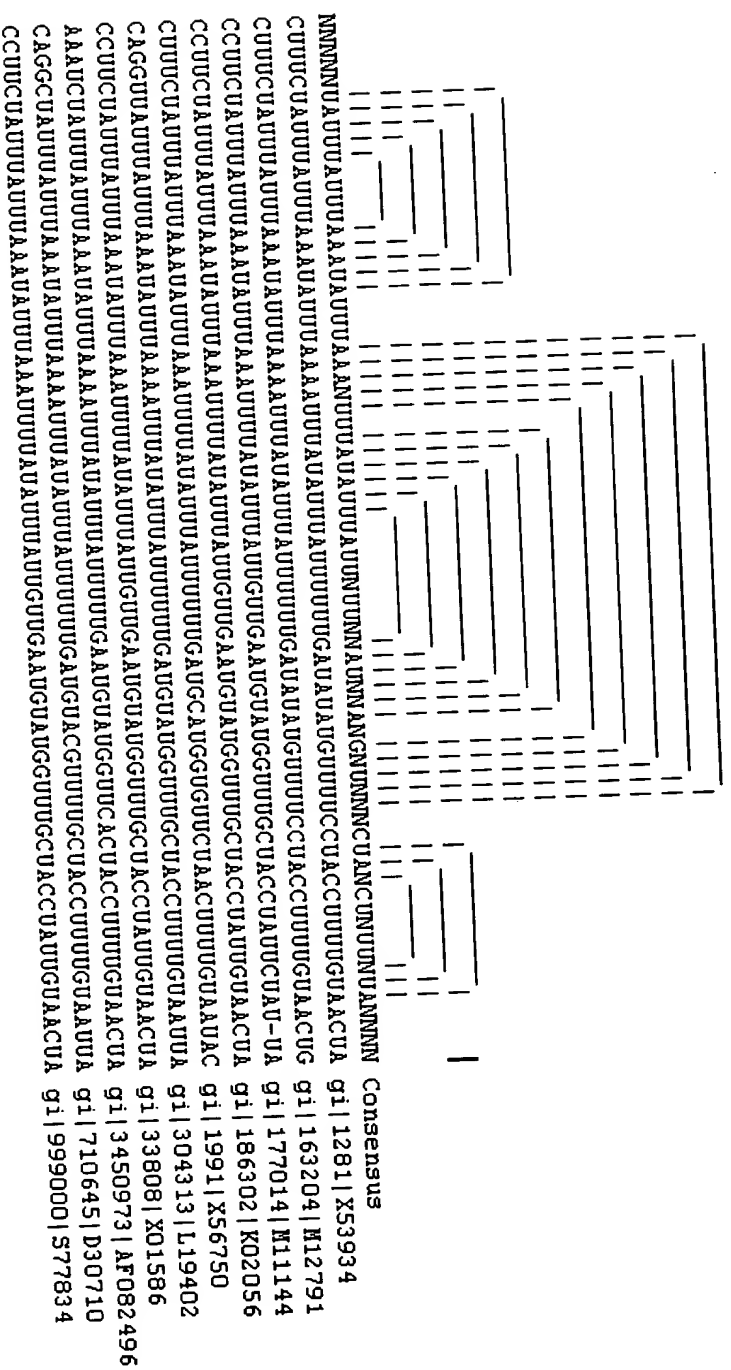
CLUSTAL W (1.74) multiple sequence alignment

```
gi|1281|X53934
gi|163204|M12791
gi|177014|M11144
gi|186302|K02056
gi|1991|X56750
gi|304313|L19402
gi|33808|X01586
gi|3450973|AF082496
gi|710645|D30710
gi|999000|S77834

CTTCTATTATTAAATATTTAAATTTATATTATTTTGGATATATGTTTCTACCTTTGTAAC
CTTCTATTATTAAATATTTAAATTTATATTATTATTTTGGATATATGTTTCTACCTTTGTAAC
CCTTCTATTATTAAATATTTAAATTTTATATTATTTGGAATGATGTTTCTACCTATTCTAT-
CCTTCTATTATTAAATATTTAAATTTTATATTATTTGGAATGATGTTTCTACCTATTGTAAC
CTTCTATTATTAAATATTTAAATTTTATATTATTATTTTGGATGCAATGTTCTAACTTTGTAAC
CAGTTATTATTAAATATTTAAATTTTATATTATTATTTTGGATGATGTTTCTACCTTTGTAAT
CCTTCTATTATTAAATATTTAAATTTTATATTATTTGGAATGATGTTTCTACCTATTGTAAC
AAATCTATTATTAAATATTTAAATTTTATATTATTATTTGGAATGATGTTTCTACCTTTGTAAC
CAGCTATTATTAAATATTTAAATTTTATATTATTATTTGGAATGATGTTTCTACCTTTGTAAT
CCTTCTATTATTAAATATTTAAATTTTATATTATTTGGAATGATGTTTCTACCTATTGTAAC
```

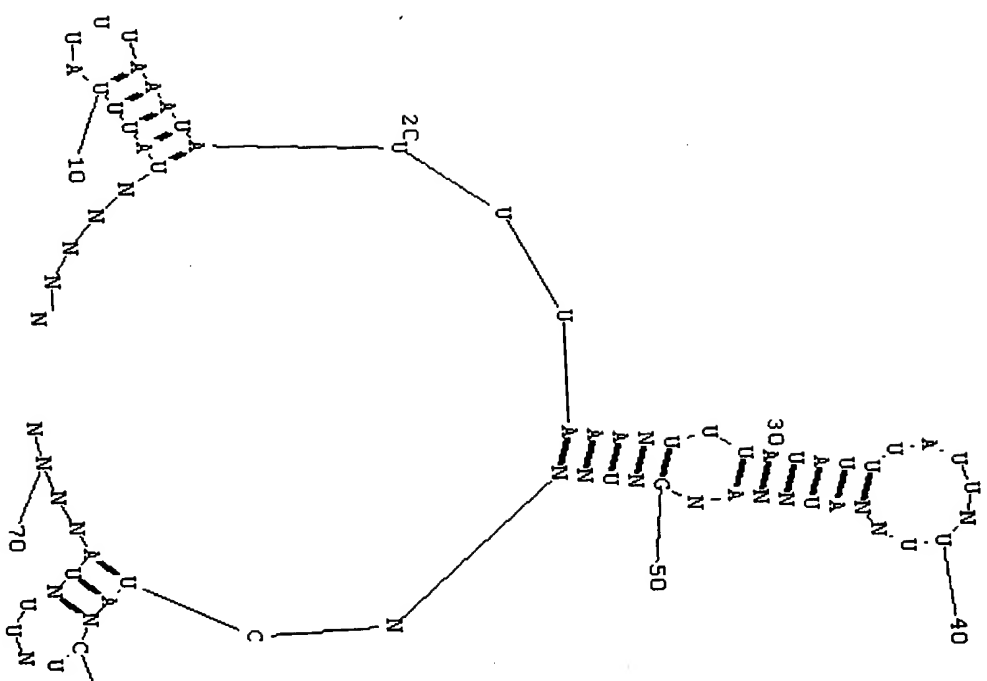
# Figure 80

Score: 404.0



09310657 : 051299

Figure 81



09310567 . 051299

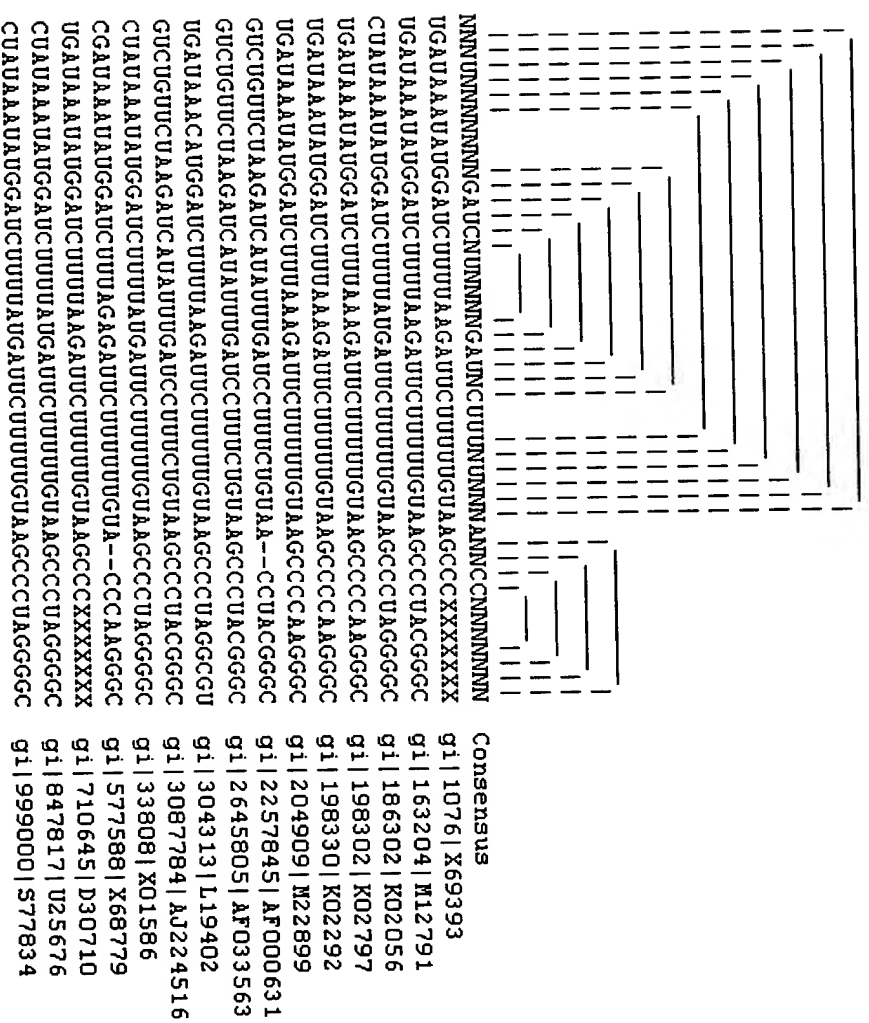
## Figure 82

CRYSTAL W (1.74) multiple sequence alignment

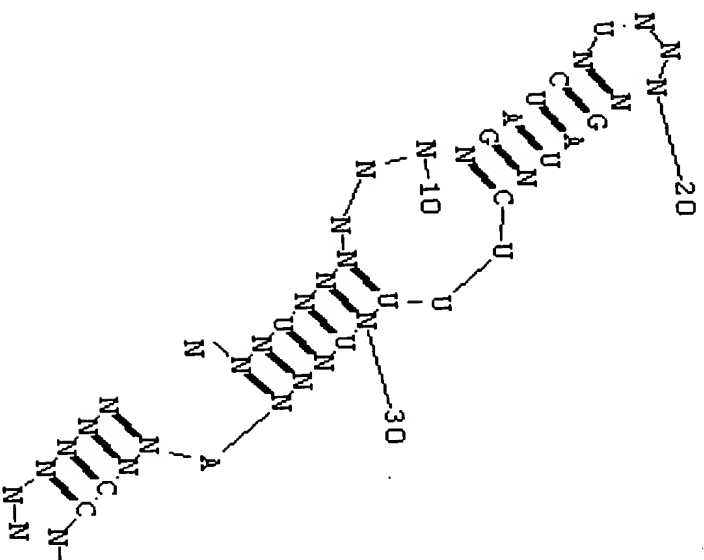
g3| 1076|X69393  
 g3| 163204|M12791  
 g3| 186300|M22005  
 g3| 186302|K02056  
 g3| 198302|K02797  
 g3| 198330|K02292  
 g3| 204909|M22899  
 g3| 2068|X58428  
 g3| 2257845|AF000631  
 g3| 2645805|AF033563  
 g3| 304313|L19402  
 g3| 3087784|AJ224516  
 g3| 33808|X01586  
 g3| 5775881|X68779  
 g3| 710645|D30710  
 g3| 847817|U25676  
 g3| 999000|S77834

Figure 83

Score: 412.0

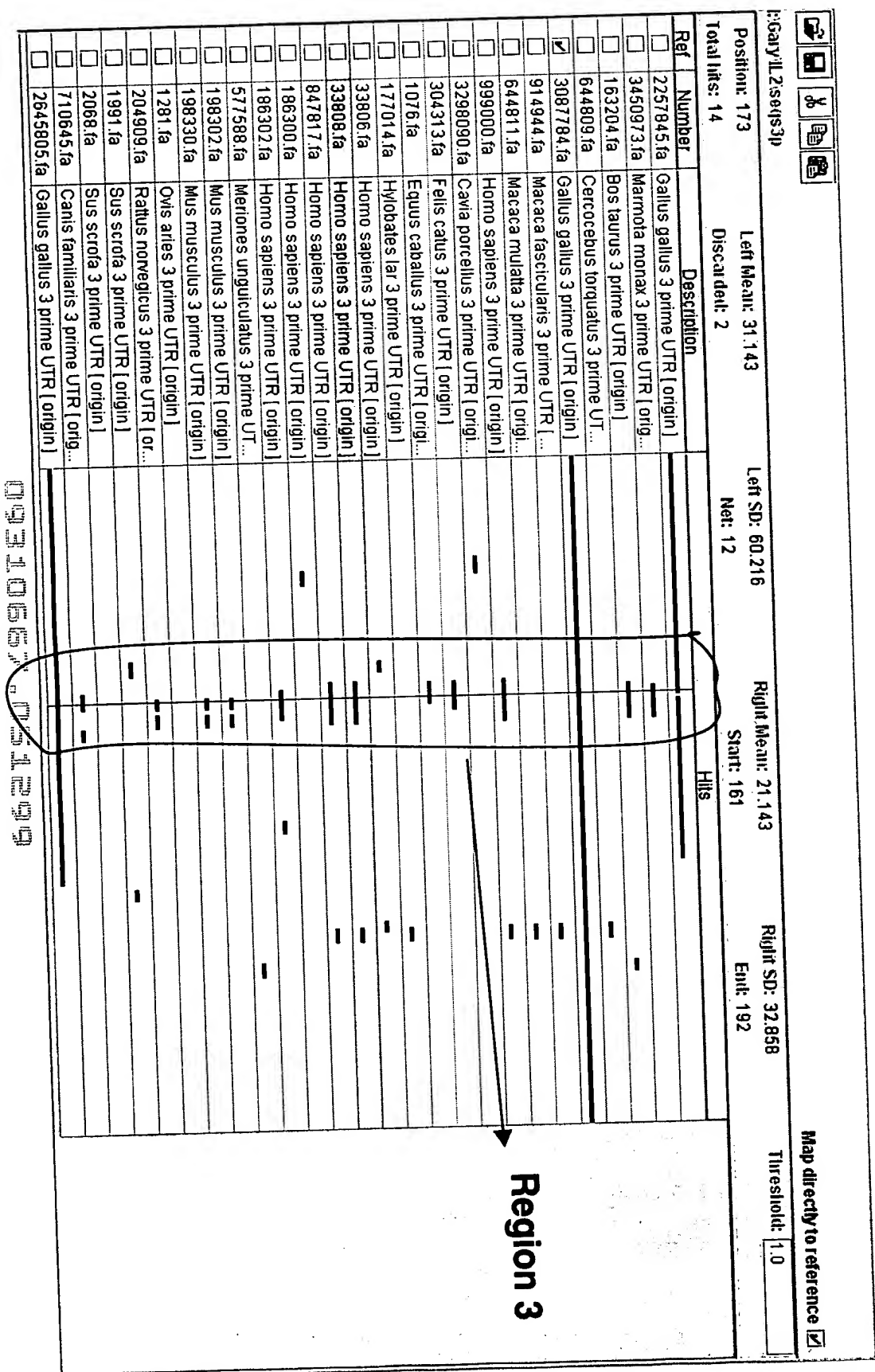


## Figure 84



0330667-051239

Figure 85





## Figure 86

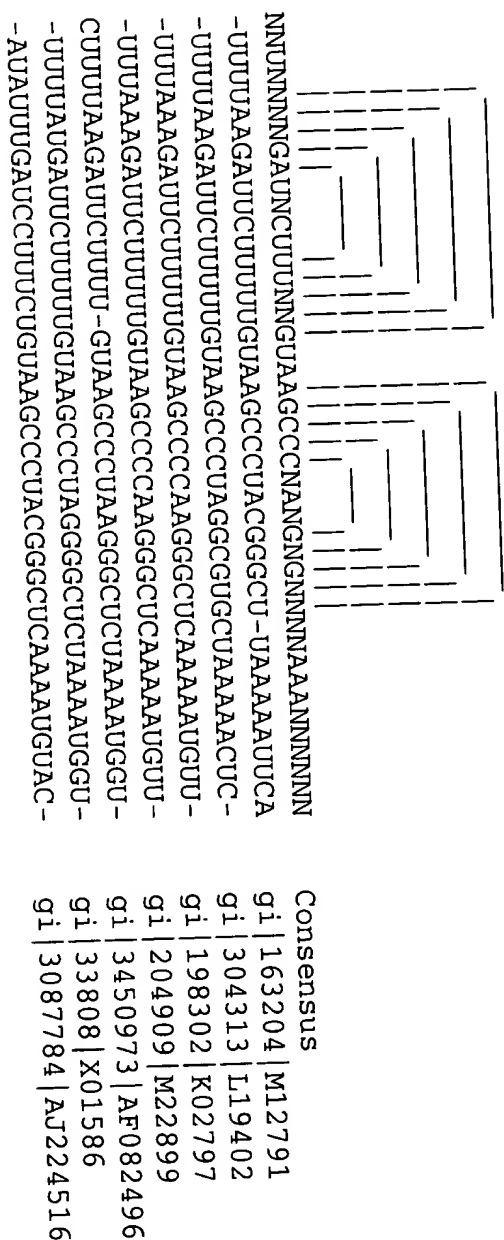
CLUSTAL W (1.74) multiple sequence alignment

```
gi|163204|M12791      -TTTAAAGATTCTTTTGTAAAGCCCTACGGCT-TAAAAATTCA
gi|304313|L19402      -TTTAAAGATTCTTTTGTAAAGCCCTAGCGCTGCTAAAAACTC-
gi|198302|K02797      -TTTAAAGATTCTTTTGTAAAGCCCAAGGCTCAAAAAATGTT-
gi|204909|M22899      -TTTAAAGATTCTTTTGTAAAGCCCAAGGCTCAAAAAATGTT-
gi|3450973|AF082496    CTTTAAAGATTCTTTT-GTAAAGCCCTAAGGCTCTAAAATGGT-
gi|33808|X01586        -TTTATGATTCTTTTGTAAAGCCCTAGGGCTCTAAAATGGT-
gi|3087784|AJ224516    -ATATTGATCCTTTCTGTAAAGCCCTACGGGCTCAAAATGTAC-
*      ***      ****      *****      *      *      ***
```

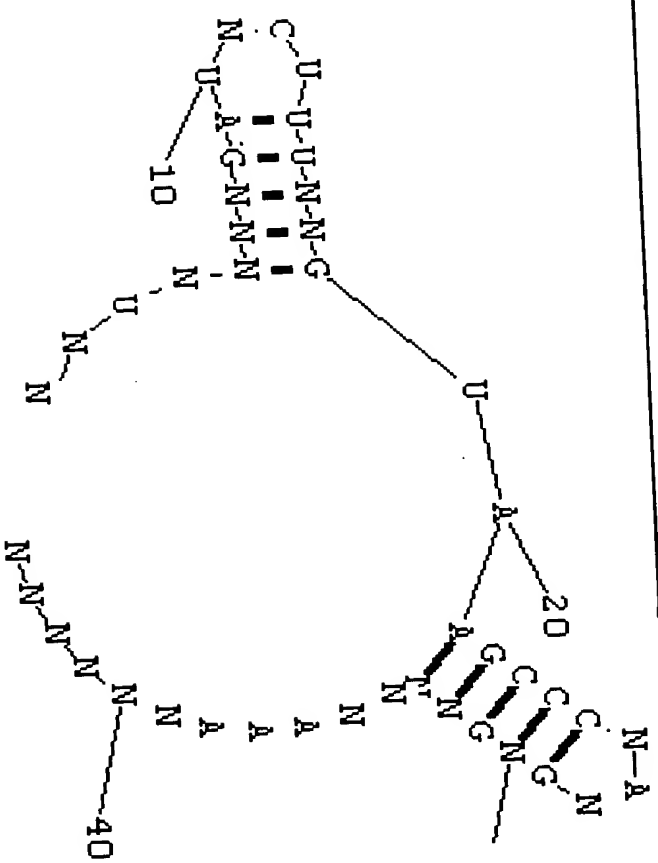
09310657.051299

Figure 87

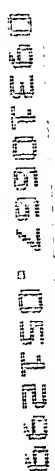
Score: 165.0



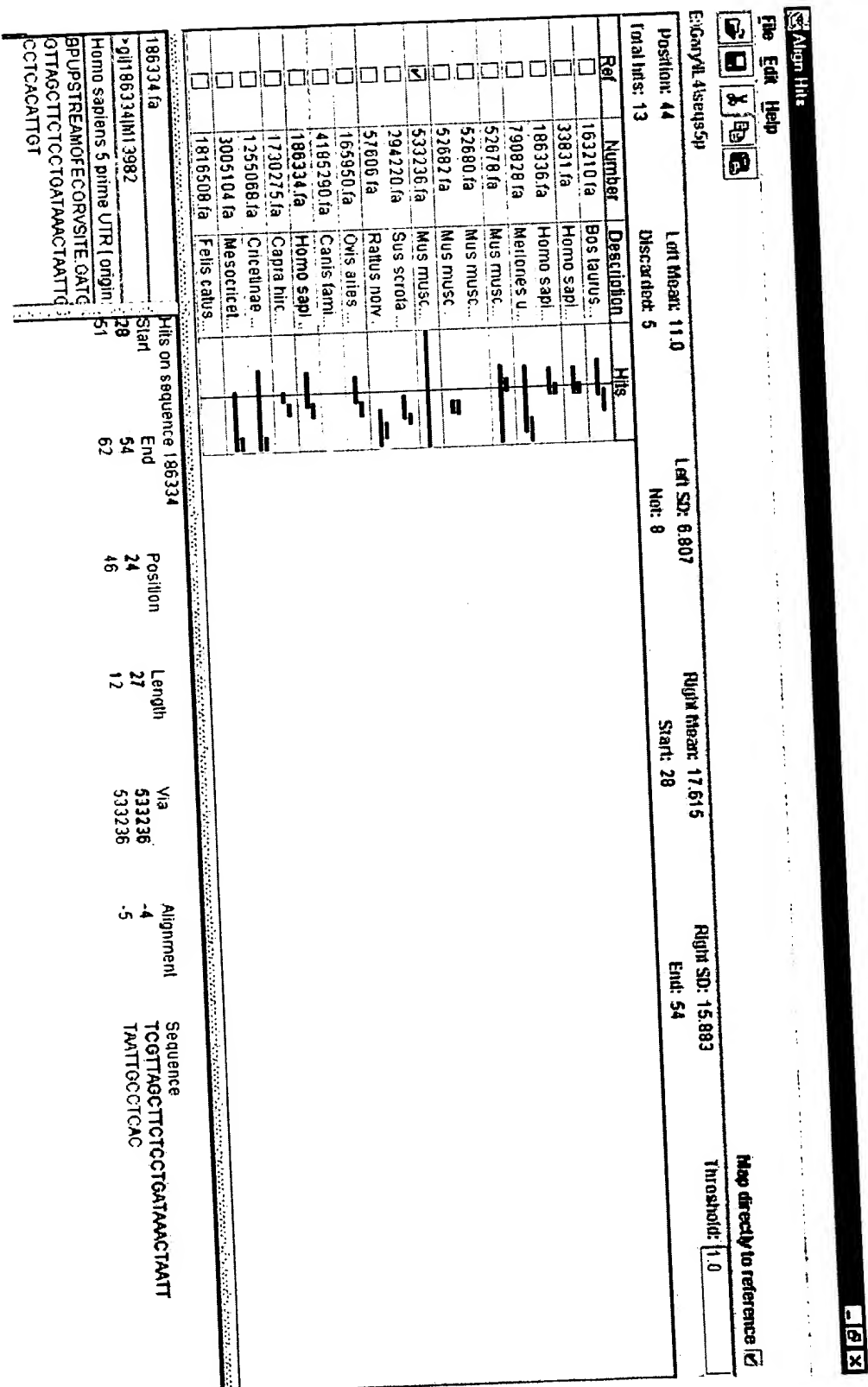
7-N



Release 34 (February 02 1999) - v.2.0 - HOVERGEN  
Interleukin 4



# Figure 90



09310567.051299

Figure 91

CLUSTAL W (1.74) multiple sequence alignment

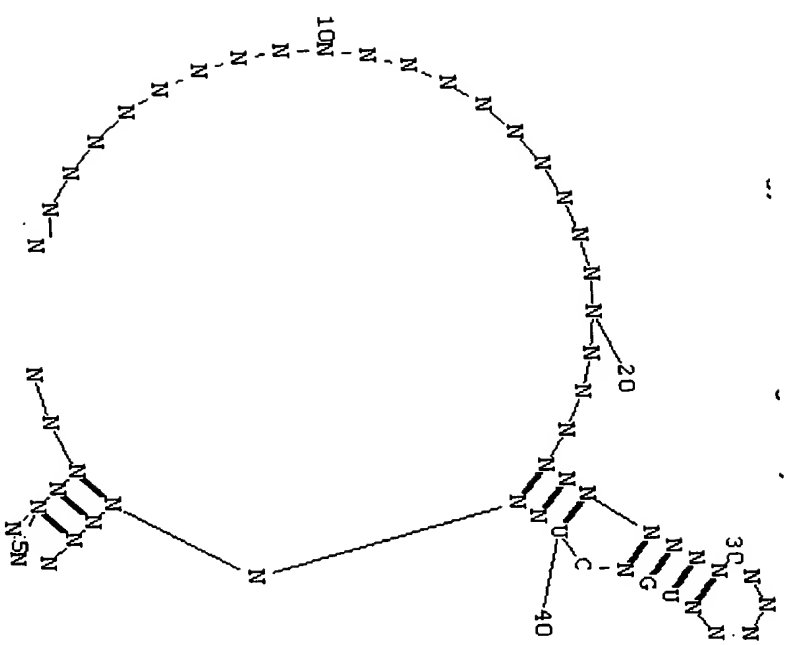
```
gi|1255068|U50415      XXXTGCAITGTTAGCGTCTCTTGATAACCTTAAT-TGTCCTATCACTGA---
gi|163210|M77120      -XXXXTGCATTTAGCGTCTCTCGTAAACTAATTGTCCTCACATTGTCAGT--
gi|165950|M96845      -XXXXXXXXXXXTAGCTTCTCTCGTGAATCTAATTGCCTCACACTGTCAGT--
gi|1730275|U34273      -XXXXXXXXXXXTAGCTTCTCTCGTGAATAACTAATTGCTCACAAGTCAAGT--
gi|1730275|U34273      -----GATCGTTAGCTTCTCTCGTGAATAACTAATTGCCCTCACATTGTXXX---
gi|186334|M13982      -GCATTCGATCGTTAGCTTCTCTCGTGAATAACTAATTGCCCTCACATGTCAGT-
gi|186336|M23442      ---XXXXXXXXXXXXXXXXXXXXGTAACCTAATTGTCCTCACATCGTCAAGTGC
gi|294220|L12991      XXXXXXXXXXXXXXXXXXXXXXTGATAACCTTAATTGTCCTCACTACTGA---
gi|3005104|AF046213    -GCATTCGATCGTTAGCTTCTCTCGTGAATAACTAATTGCCCTCACATTGTCAGT-
gi|33831|X06750      GCATTCGATTTGTTAGCATCTCTTGATAAACTTAATTGTCCTCTCGTCACTGA---
gi|52678|X05064      -GTGTCGCAAGCCAGACTTCTTGATA-TTACTCTGTCTTTCCCCAGGGCGA-
gi|52678|X05064b      XXXXXXXXXXXCCAGCCCGACAGCGAGACCCAAATCTGTCACAAATGAAC---
gi|52682|X05253      GGGGGAATTTGTTAGCATCTCTTGATAAACTTAATTGTCCTCTCGTCACTGA---
gi|533236|M25892      XXXXXXXAATGTTGCACTCTTGACAACTTAATTGTCCTCACATCCCTGA---
gi|790828|L37779
```

[illegible]

gi|1255068|U50415  
gi|163210|M77120  
gi|165950|M96845  
gi|1730275|U34273  
gi|186334|M13982  
gi|186336|M23442  
gi|294220|L12991  
gi|3005104|AF046213  
gi|33831|X06750  
gi|52678|X05064  
gi|52678|X05064b  
gi|52682|X05253  
gi|533236|M25892  
gi|790828|L37779

[illegible]

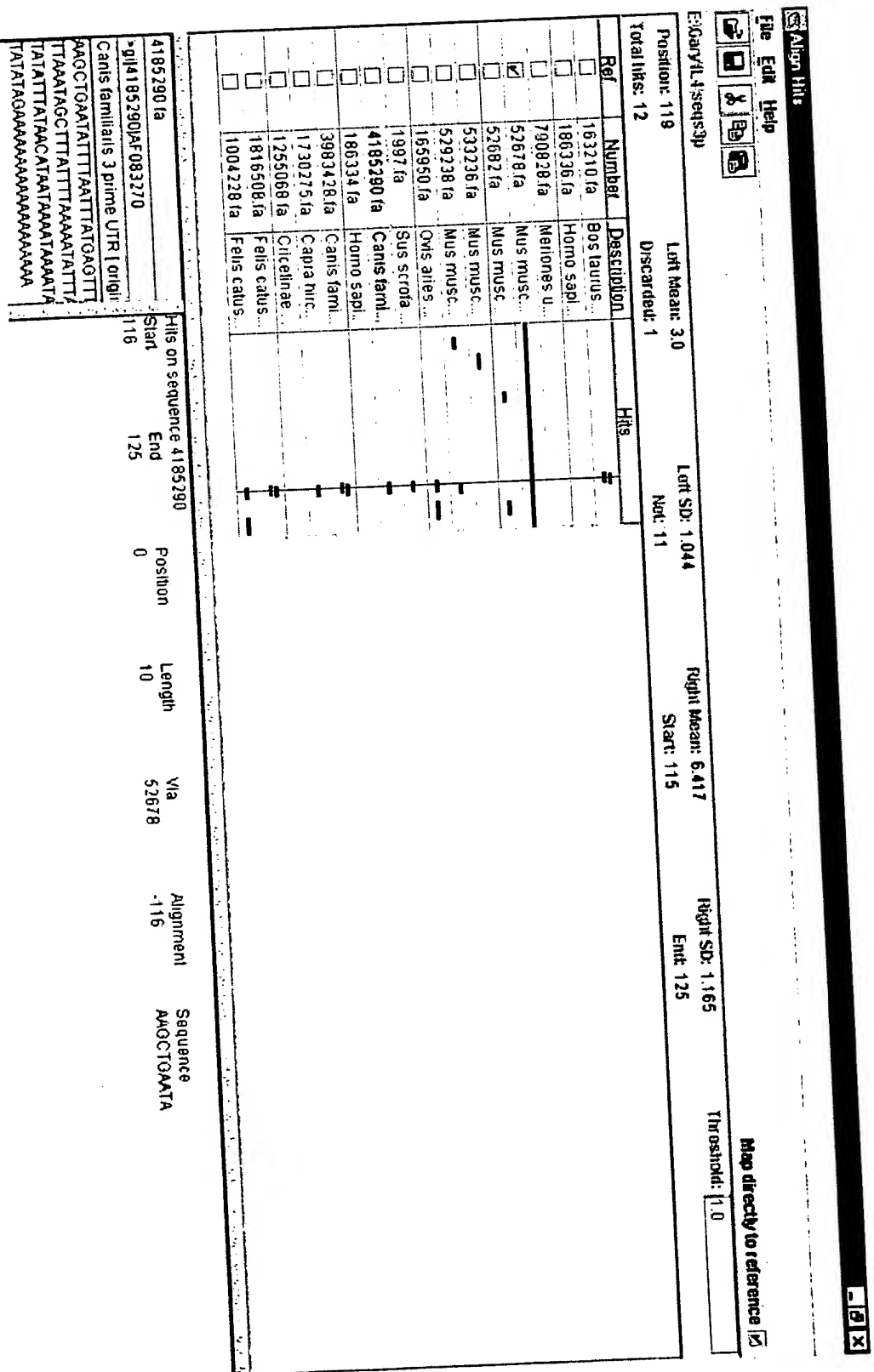
Figure 93



09310667.051299



# Figure 94



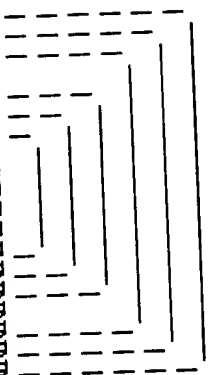
# Figure 95

CLUSTAL W (1.74) multiple sequence alignment

```
gi| 1004228|X87408      TTATAATTATTATAAATAAGTATATGT-
gi| 1004228|X87408b    XXXXXAAGCTGAATATCTTAATTATGAG
gi| 163210|M77120      ATGTAGAGCTGAAAAAAXXXXXXXXXXX
gi| 163210|M77120b    XXXXXAAGCTGAATATTTAATTATGAG
gi| 165950|M96845      AATTATGCTTTTAAATAGCTTATAT---
gi| 165950|M96845b    XXXXXAAGCTGAATATTTAATTATGAC
gi| 1730275|U34273     XXXXXAAGCTGAATATTTAATTATGAC
gi| 1816508|U39634     ATGTAGAACTGAAAAAAXXXXXXXXXAA
gi| 1816508|U39634b   XXXXXAAGCTGAATATCTTAATTATGAG
gi| 19971X68330        XXXXXAAGCTGACTATTTTAATTATGAT
gi| 3983428|AF104245   ATATAGACCTAAAAAAXXXXXXXXXXX
gi| 3983428|AF104245b XXXXXAAGCTGAATATTTTAATTATGAG
gi| 4185290|AF083270   XXXXXAAGCTGAATATTTTAATTATGAG
gi| 52678|X05064       ACACGAATCTGAATGAGAAATGCCGTGAT
gi| 52682|X05253       ACTTCATTGCCATAAGGTTCTACTGTTAG
gi| 529238|L32955      ATAAAAAACAAACTTCCXXXXXXXXXX
gi| 529238|L32955b    GTGTCCCACTGAAGGAGCAAGGCTCAGGC
```

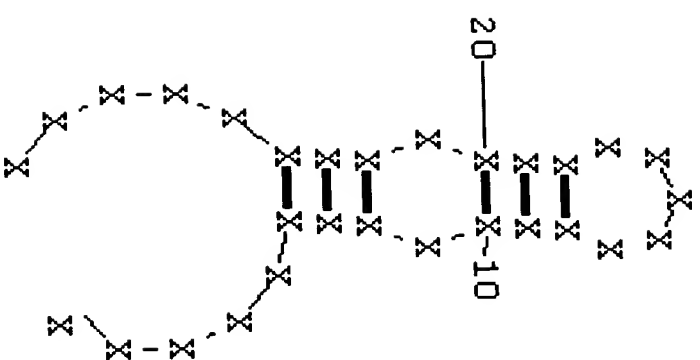
# Figure 96

Score: 136.0

[illegible]

031057 0710

Figure 97



09310657.051299